

STIC-Biotech/ChemLib

8-543

198333

ME

From: Jiang, Dong
Sent: Thursday, August 10, 2006 8:01 PM
To: STIC-Biotech/ChemLib
Subject: 10/735,149

Please search SEQ ID NO:28, and 27.

- issued & Pub.
- commercial

Please send results on paper to Dong Jiang in REM 4D70 (mail stop REM 4C70).

Thank you very much.

Dong

Dong Jiang

AU1646
REM - 4D70
571-272-0872
Mail stop REM - 4C70

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

THIS PAGE LEFT BLANK

Db 382 AAAAAACACCCAAAGATTCCTAGAAAGATTCCTCAATACCTTCACAAAAGATTCAT 441
 QY 364 CAGCAGCTGCTCTCTCTGACCCAGCGTTCGGAAGATTCCTGA 405
 Db 442 CAGCATCTGCTCTCTAGAACACAGGAAGTGAAGATTCCTGA 483

RESULT 4

US-09-949-016-4436
 ; Sequence 4436, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; FILE REFERENCE: C1001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4436
 ; LENGTH: 623
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-4436

Query Match 74.0%; Score 299.6; DB 3; Length 623;
 Best Local Similarity 84.1%; Pred. No. 2.9e-87;
 Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 4 CAAGGTCAAGATCGCCACATGATTAGAAATGCGTCACTTATAGATTTGATGACGCTG 63
 Db 134 CAAGGTCAAGATCGCCACATGATTAGAAATGCGTCACTTATAGATTTGATGACGCTG 193
 QY 64 AAAAAATATGATGATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 123
 Db 194 AAAAAATATGATGATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 253
 QY 124 AACTGTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 183
 Db 254 AACTGTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 313
 QY 184 GGTAAACAGACGATCATCAACGTTTCAATTAATAAAGTAAACGTCGCTCC 243
 Db 314 GGAACATGAAAGATTAATCAATGATTAATAAAGTAAAGGAAAGAAACCACTTCC 373
 QY 244 ACCAAGCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 303
 Db 374 ACAATGACAGGAGAAAGACAGAAACAGACTAACTAGCCCTTATGATTTCTTAAGAG 433
 QY 304 AAAAAACCGCCGAAAGAAATTCCTGGAACGTTTCAATCCCTGCTGCAAGAAATGATTCAC 363
 Db 434 AAAAAACCGCCGAAAGAAATTCCTGGAACGTTTCAATCCCTGCTGCAAGAAATGATTCAT 493
 QY 364 CAGCAGCTGCTCTCTCTGACCCAGCGTTCGGAAGATTCCTGA 405
 Db 494 CAGCATCTGCTCTCTAGAACACAGGAAGTGAAGATTCCTGA 535

RESULT 5

US-09-522-217-1
 ; Sequence 1, Application US/09522217
 ; Patent No. 6307024
 ; GENERAL INFORMATION:
 ; APPLICANT: No. 6307024ak, Julia E.
 ; APPLICANT: Presnell, Scott R.

APPLICANT: Sprecher, Cindy A.
 APPLICANT: Foster, Donald C.
 APPLICANT: Holly, Richard D.
 APPLICANT: Gross, Jane A.
 APPLICANT: Johnston, Janet V.
 APPLICANT: Nelson, Andrew J.
 APPLICANT: Dillon, Stacey R.
 APPLICANT: Hammond, Angela R.
 TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND
 FILE REFERENCE: 99-16
 CURRENT APPLICATION NUMBER: US/09/522,217
 CURRENT FILING DATE: 2000-03-09
 EARLIER APPLICATION NUMBER: US 60/123,547
 EARLIER FILING DATE: 1999-03-09
 EARLIER APPLICATION NUMBER: US 60/123,904
 EARLIER FILING DATE: 1999-03-11
 EARLIER APPLICATION NUMBER: US 60/142,013
 EARLIER FILING DATE: 1999-07-01
 NUMBER OF SEQ ID NOS: 115
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 1
 LENGTH: 642
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (47) ... (532)
 US-09-522-217-1

Query Match 74.0%; Score 299.6; DB 3; Length 642;
 Best Local Similarity 84.1%; Pred. No. 2.9e-87;
 Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 4 CAAGGTCAAGATCGCCACATGATTAGAAATGCGTCACTTATAGATTTGATGACGCTG 63
 Db 134 CAAGGTCAAGATCGCCACATGATTAGAAATGCGTCACTTATAGATTTGATGACGCTG 193
 QY 64 AAAAAATATGATGATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 123
 Db 194 AAAAAATATGATGATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 253
 QY 124 AACTGTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 183
 Db 254 AACTGTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 313
 QY 184 GGTAAACAGACGATCATCAACGTTTCAATTAATAAAGTAAACGTCGCTCC 243
 Db 314 GGAACATGAAAGATTAATCAATGATTAATAAAGTAAAGGAAAGAAACCACTTCC 373
 QY 244 ACCAAGCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 303
 Db 374 ACAATGACAGGAGAAAGACAGAAACAGACTAACTAGCCCTTATGATTTCTTAAGAG 433
 QY 304 AAAAAACCGCCGAAAGAAATTCCTGGAACGTTTCAATCCCTGCTGCAAGAAATGATTCAC 363
 Db 434 AAAAAACCGCCGAAAGAAATTCCTGGAACGTTTCAATCCCTGCTGCAAGAAATGATTCAT 493
 QY 364 CAGCAGCTGCTCTCTCTGACCCAGCGTTCGGAAGATTCCTGA 405
 Db 494 CAGCATCTGCTCTCTAGAACACAGGAAGTGAAGATTCCTGA 535

RESULT 6

US-09-923-246-1
 ; Sequence 1, Application US/09923246
 ; Patent No. 605272
 ; GENERAL INFORMATION:
 ; APPLICANT: No. 605272ak, Julia E.
 ; APPLICANT: Presnell, Scott R.
 ; APPLICANT: Sprecher, Cindy A.
 ; APPLICANT: Foster, Donald C.
 ; APPLICANT: Holly, Richard D.
 ; APPLICANT: Gross, Jane A.

THIS PAGE LEFT BLANK

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2006, 12:10:09 ; Search time 150 Seconds
(without alignments)
5051.994 Million cell updates/sec

Title: US-10-735-149-27

Perfect score: 405
Sequence: 1 atgaagctcagatcgcca.....acggtccgaatctctga 405

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PTCUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	299.6	74.0	483	3	US-09-522-217-63 Sequence 63, Appl
2	299.6	74.0	483	3	US-09-923-246-63 Sequence 63, Appl
3	299.6	74.0	483	3	US-10-295-723-63 Sequence 63, Appl
4	299.6	74.0	623	3	US-09-949-016-4436 Sequence 4436, Ap
5	299.6	74.0	642	3	US-09-522-217-1 Sequence 1, Appl
6	299.6	74.0	642	3	US-09-923-246-1 Sequence 1, Appl
7	299.6	74.0	642	3	US-10-295-723-1 Sequence 1, Appl
8	299.6	74.0	642	3	US-10-282-622-1 Sequence 1, Appl
9	299.6	73.2	486	3	US-09-825-561A-9 Sequence 9, Appl
10	294.8	72.8	489	3	US-10-282-622-5 Sequence 5, Appl
11	293.6	72.5	1560	3	US-09-522-217-84 Sequence 84, Appl
12	293.6	72.5	1560	3	US-09-923-246-84 Sequence 84, Appl
13	293.6	72.5	1560	3	US-10-295-723-84 Sequence 84, Appl
14	290.6	71.8	486	3	US-09-522-217-3 Sequence 3, Appl
15	290.6	71.8	486	3	US-09-923-246-3 Sequence 3, Appl
16	290.6	71.8	486	3	US-10-295-723-3 Sequence 3, Appl
17	264.4	65.3	444	3	US-10-282-622-3 Sequence 3, Appl
18	182	44.9	3072	3	US-09-522-217-55 Sequence 55, Appl
19	182	44.9	3072	3	US-09-923-246-55 Sequence 55, Appl
20	182	44.9	3072	3	US-10-295-723-55 Sequence 55, Appl
21	182	44.9	3072	3	US-09-825-561A-46 Sequence 46, Appl
22	175	43.2	1533	3	US-09-522-217-88 Sequence 88, Appl
23	175	43.2	1533	3	US-09-923-246-88 Sequence 88, Appl

24	175	43.2	1533	3	US-10-295-723-88 Sequence 88, Appl
25	105	25.9	12437	3	US-09-949-016-16178 Sequence 16178, A
26	103.4	25.5	1656	3	US-09-522-217-106 Sequence 106, App
27	103.4	25.5	1656	3	US-09-923-246-106 Sequence 106, App
28	103.4	25.5	1656	3	US-10-295-723-106 Sequence 106, App
29	81.4	20.1	1347	3	US-09-522-217-105 Sequence 105, App
30	81.4	20.1	1347	3	US-09-923-246-105 Sequence 105, App
31	81.4	20.1	1347	3	US-10-295-723-105 Sequence 105, App
32	59.6	14.7	535	3	US-09-522-217-4 Sequence 4, Appl
33	59.6	14.7	535	3	US-09-923-246-4 Sequence 4, Appl
34	59.6	14.7	535	3	US-10-295-723-4 Sequence 108, App
35	58.8	14.5	645	3	US-09-522-217-108 Sequence 108, App
36	58.8	14.5	645	3	US-09-923-246-108 Sequence 108, App
37	58.8	14.5	645	3	US-10-295-723-108 Sequence 108, App
38	44.4	11.0	601	3	US-09-949-016-15862 Sequence 15862, A
39	35.2	8.7	40465	3	US-09-949-016-15561 Sequence 12561, A
40	32	7.9	1600	3	US-09-949-016-4038 Sequence 4038, Ap
41	32	7.9	12113	3	US-09-949-016-15144 Sequence 15144, A
42	32	7.9	13445	3	US-09-949-016-15780 Sequence 15780, A
43	31.6	7.8	73853	3	US-09-949-016-12029 Sequence 12029, A
44	31.4	7.8	1230230	3	US-09-438-185A-1 Sequence 1, Appl
45	31.2	7.7	6819	3	US-09-949-016-12457 Sequence 12457, A

ALIGNMENTS

RESULT 1	
US-09-522-217-63	
Sequence 63, Application US/09522217	
Patent No. 6307024	
GENERAL INFORMATION:	
APPLICANT: No. 6307024ak, Julia E.	
APPLICANT: Presnell, Scott R.	
APPLICANT: Sprecher, Cindy A.	
APPLICANT: Foster, Donald C.	
APPLICANT: Holly, Richard D.	
APPLICANT: Gross, Jane A.	
APPLICANT: Johnston, Janet V.	
APPLICANT: Nelson, Andrew J.	
APPLICANT: Dillon, Stacey R.	
APPLICANT: Hammond, Angela K.	
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND	
FILE REFERENCE: 99-16	
CURRENT APPLICATION NUMBER: US/09/522.217	
CURRENT FILING DATE: 2000-03-09	
EARLIER APPLICATION NUMBER: US 60/123.547	
EARLIER FILING DATE: 1999-03-09	
EARLIER APPLICATION NUMBER: US 60/123.904	
EARLIER FILING DATE: 1999-03-11	
EARLIER APPLICATION NUMBER: US 60/142.013	
EARLIER FILING DATE: 1999-07-01	
NUMBER OF SEQ ID NOS: 115	
SOFTWARE: FastSeq for Windows Version 3.0	
SEQ ID NO 63	
LENGTH: 483	
TYPE: DNA	
ORGANISM: homo sapiens	
US-09-522-217-63	
Query Match	74.0%; Score 299.6; DB 3; Length 483;
Best Local Similarity	84.1%; Pred. No. 2.6e-87;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;	
OY 4 CAAGTCAAGTGGCCACATGATTGAATGCGTCAACTTATGATATTGATCAGCTG 63	
DB 82 CAAGTCAAGTGGCCACATGATTGAATGCGTCAACTTATGATATTGATCAGCTG 141	
OY 64 AAAAATTATGATGAATGATGATGCTTCCGGAATTTCTGCGGCTCCGGAAGATGTTGAGACC 123	
DB 142 AAAAATTATGATGAATGATGATGCTTCCGGAATTTCTGCGGCTCCGGAAGATGTTGAGACA 201	
OY 124 AACTGTGATGCTGCTGCTTTCTCTCTTTCCAGAAAGCCAGCTGAATTCGCAAAACACC 183	

```
|||||
Db 202 AACTGTAGTGTGACGTTTCTCTGTTTTCAGAGGCCCACTAAAGTCAGCAAAATACA 261
Qy 184 GGTAAACGACGATCATCAACGTTCCATTAAAACTGAAACGTAAACCGCCGTC 243
Db 262 GGAACCAATGAAAGATTAATCAATGTATCAATTAAGCTGAAAGAAACCACTTCC 321
Qy 244 ACCAAGCAGAGTGTGCTGCAAAAACCGTCTGACCGCCGTCCTGTGATTCTATGAG 303
Db 322 ACAATGCAAGGAGAAACAGAAACACAGACTAATCATGCCCTTCATGTGATTTATGAG 381
Qy 304 AAAAAACCGCCGAAAGAAATTCCTGAAACGTTTCAAAATCCCTGTGACAGAAATGATTAC 363
Db 382 AAAAAACCAACCAAGAAATTCCTAGAAAGATTCAAATCACTTCCAAAAAGATGATTCAT 441
Qy 364 CAGCAGCTGTCTCTGCTGATCCCAACGGTTCGGAATGCTGA 405
Db 442 CAGCATCTGTCTCTAGAACACACGGAAGTGAAGATTCCTGA 483
```

RESULT 2

```
US-09-923-246-63
; Sequence 63, Application US/09923246
; Patent No. 6605272
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey K.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA1 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923, 246
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522, 217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123, 904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142, 013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 483
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-923-246-63
```

```
Query Match 74.0%; Score 299.6; DB 3; Length 483;
Best Local Similarity 84.1%; Pred. No. 2,6e-87;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
```

```
Qy 4 CAAGTCAAGATCGCCACATGATTAGAAATGCGTCACTTATAGATTTGTTGATCAGCTG 63
Db 82 CAAGTCAAGATCGCCACATGATTAGAAATGCGTCACTTATAGATTTGTTGATCAGCTG 141
Qy 64 AAAAAATATGTGAATGACCTGTTCCGGAATTCCTGCCGCGTCCGGAAGATGTTGAAC 123
Db 142 AAAAAATATGTGAATGACCTGTTCCGGAATTCCTGCCGCGTCCGGAAGATGTTGAAC 201
Qy 124 AACTGTAGTGTGCGCTTTCTCTGTTTCCAGAAAGCCGAGTGAATCCGCAAAACACC 183
Db 202 AACTGTAGTGTGCGCTTTCTCTGTTTCCAGAAAGCCGAGTGAATCCGCAAAACACC 261
Qy 184 GGTAAACGACGATCATCAACGTTTCCATTAAAACTGAAACGTAAACCGCCGTC 243
Db 262 GGAACCAATGAAAGATTAATCAATGTATCAATTAAGCTGAAAGAAACCACTTCC 321
```

```
Qy 244 ACCAAGCAGAGTGTGCTGCAAAAACCGTCTGACCTGCCGTCCTGTGATTCCTATGAG 303
Db 322 ACAATGCAAGGAGAAACAGAAACACAGACTAATCATGCCCTTCATGTGATTTATGAG 381
Qy 304 AAAAAACCGCCGAAAGAAATTCCTGAAACGTTTCAAAATCCCTGTGACAGAAATGATTAC 363
Db 382 AAAAAACCAACCAAGAAATTCCTAGAAAGATTCAAATCACTTCCAAAAAGATGATTCAT 441
Qy 364 CAGCAGCTGTCTCTGCTGATCCCAACGGTTCGGAATGCTGA 405
Db 442 CAGCATCTGTCTCTAGAACACACGGAAGTGAAGATTCCTGA 483
```

RESULT 3

```
US-10-295-723-63
; Sequence 63, Application US/10295723
; Patent No. 6686178
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey K.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA1 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295, 723
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522, 217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123, 547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123, 904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142, 013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 483
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-295-723-63
```

```
Query Match 74.0%; Score 299.6; DB 3; Length 483;
Best Local Similarity 84.1%; Pred. No. 2,6e-87;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
```

```
Qy 4 CAAGTCAAGATCGCCACATGATTAGAAATGCGTCACTTATAGATTTGTTGATCAGCTG 63
Db 82 CAAGTCAAGATCGCCACATGATTAGAAATGCGTCACTTATAGATTTGTTGATCAGCTG 141
Qy 64 AAAAAATATGTGAATGACCTGTTCCGGAATTCCTGCCGCGTCCGGAAGATGTTGAAC 123
Db 142 AAAAAATATGTGAATGACCTGTTCCGGAATTCCTGCCGCGTCCGGAAGATGTTGAAC 201
Qy 124 AACTGTAGTGTGCGCTTTCTCTGTTTCCAGAAAGCCGAGTGAATCCGCAAAACACC 183
Db 202 AACTGTAGTGTGCGCTTTCTCTGTTTCCAGAAAGCCGAGTGAATCCGCAAAACACC 261
Qy 184 GGTAAACGACGATCATCAACGTTTCCATTAAAACTGAAACGTAAACCGCCGTC 243
Db 262 GGAACCAATGAAAGATTAATCAATGTATCAATTAAGCTGAAAGAAACCACTTCC 321
Qy 244 ACCAAGCAGAGTGTGCTGCAAAAACCGTCTGACCTGCCGTCCTGTGATTCCTATGAG 303
Db 322 ACAATGCAAGGAGAAACAGAAACACAGACTAATCATGCCCTTCATGTGATTTATGAG 381
Qy 304 AAAAAACCGCCGAAAGAAATTCCTGAAACGTTTCAAAATCCCTGTGACAGAAATGATTAC 363
```

Db 382 AAAAAAAAAAAGGATTTCTTGAAGATTCATCTTCCAAAGATGATTCAT 441
Qy 364 CAGACCTGTCTCTCGTACCCAGGTTCCGAAGATTCCTGA 405
Db 442 CAGATCTGTCTCTTGAAGACACGGAAGTGAAGATTCCTGA 483

RESULT 4
US-09-949-016-4436

Sequence 4436, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4436
LENGTH: 623
TYPE: DNA
ORGANISM: Human
US-09-949-016-4436

Query Match 74.0%; Score 299.6; DB 3; Length 623;
Best Local Similarity 84.1%; Pred. No. 2.9e-87;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 4 CAAGGTCAAGATCGCCACATGATTAGAAATGCGTCACTTATAGATTTGATCAGCTG 63
Db 134 CAAGGTCAAGATCGCCACATGATTAGAAATGCGTCACTTATAGATTTGATCAGCTG 193
Qy 64 AAAAAATTTATGTAATGACCTGTTCCGGAATTCCTCCGCGCTCCGGAAGATTTGAGACC 123
Db 194 AAAAAATTTATGTAATGACCTGTTCCGGAATTTCTGCAAGATGTTAGAGACA 253
Qy 124 AACTGTGAGTGTCCGCTTTCTCTGTTCCAGAAAGCCAGCTGAAATCCGCAACACC 183
Db 254 AACTGTGAGTGTCCGCTTTCTCTGTTCCAGAAAGCCAGCTGAAATCCGCAACACC 313
Qy 184 GGTAAACAAGACGATATCATCAACGTTTCAATTAATAAACTGAAACGTAACCCGCGCTCC 243
Db 314 GGAACCAATGAAAGATATCATATGATTAATAAAAGCTGAAGAGAAACCACTTCC 373
Qy 244 ACCAAGCAGAGTGTCTGTCAAGAAACAGCTGACCTGCGCTGATTTCTTATGAG 303
Db 374 ACAATGCAAGGAGAGAAAGACAGAAACAAGATCAATGATTTCTTATGAG 433
Qy 304 AAAAAACCGCGGAAGATTTCTGGAAGCTTCAATCCGCTGACAGAAATGATTCAC 363
Db 434 AAAAAACCAACCAAGATTTCTTGAAGATTTCAATCACTTCTCAAAAGATGATTCAT 493
Qy 364 CAGACCTGTCTCTCTGTACCAAGGTTCCGAAGATTCCTGA 405
Db 494 CAGATCTGTCTCTTGAAGACACGGAAGTGAAGATTCCTGA 535

RESULT 5
US-09-522-217-1

Sequence 1, Application US/09522217
Patent No. 6307024
GENERAL INFORMATION:
APPLICANT: No. 6307024ak, Julia E.
APPLICANT: Presnell, Scott R.

APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/522,217
CURRENT FILING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: US 60/142,013
EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 642
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (47)...(532)
US-09-522-217-1

Query Match 74.0%; Score 299.6; DB 3; Length 642;
Best Local Similarity 84.1%; Pred. No. 2.9e-87;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 4 CAAGGTCAAGATCGCCACATGATTAGAAATGCGTCACTTATAGATTTGATCAGCTG 63
Db 134 CAAGGTCAAGATCGCCACATGATTAGAAATGCGTCACTTATAGATTTGATCAGCTG 193
Qy 64 AAAAAATTTATGTAATGACCTGTTCCGGAATTCCTCCGCGCTCCGGAAGATTTGAGACC 123
Db 194 AAAAAATTTATGTAATGACCTGTTCCGGAATTTCTGCAAGATGTTAGAGACA 253
Qy 124 AACTGTGAGTGTCCGCTTTCTCTGTTCCAGAAAGCCAGCTGAAATCCGCAACACC 183
Db 254 AACTGTGAGTGTCCGCTTTCTCTGTTCCAGAAAGCCAGCTGAAATCCGCAACACC 313
Qy 184 GGTAAACAAGACGATATCATCAACGTTTCAATTAATAAACTGAAACGTAACCCGCGCTCC 243
Db 314 GGAACCAATGAAAGATATCATATGATTAATAAAAGCTGAAGAGAAACCACTTCC 373
Qy 244 ACCAAGCAGAGTGTCTGTCAAGAAACAGCTGACCTGCGCTGATTTCTTATGAG 303
Db 374 ACAATGCAAGGAGAGAAAGACAGAAACAAGATCAATGATTTCTTATGAG 433
Qy 304 AAAAAACCGCGGAAGATTTCTGGAAGCTTCAATCCGCTGACAGAAATGATTCAC 363
Db 434 AAAAAACCAACCAAGATTTCTTGAAGATTTCAATCACTTCTCAAAAGATGATTCAT 493
Qy 364 CAGACCTGTCTCTCTGTACCAAGGTTCCGAAGATTCCTGA 405
Db 494 CAGATCTGTCTCTTGAAGACACGGAAGTGAAGATTCCTGA 535

RESULT 6
US-09-923-246-1

Sequence 1, Application US/09923246
Patent No. 6605272
GENERAL INFORMATION:
APPLICANT: No. 6605272ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.

RESULT 7
US-10-295-723-1
: Sequence 1, Application US/10295723
: Patent No. 6686178
: GENERAL INFORMATION:
: APPLICANT: No. 6686178ak, Julia E.
: APPLICANT: Presnell, Scott R.
: APPLICANT: Speecher, Cindy A.
: APPLICANT: Foster, Donald C.
: APPLICANT: Holly, Richard D.
: APPLICANT: Gross, Jane A.
: APPLICANT: Johnson, Janet V.
: APPLICANT: Nelson, Andrew J.
: APPLICANT: Dillon, Stacey R.
: APPLICANT: Hammond, Angela K.

```

RESULT 8
US-10-282-622-1
; Sequence 1, Application US/10282622
; Patent No. 6929932
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: West, James W.
; APPLICANT: No. 6929932ak, Julia E.
; TITLE OF INVENTION: ZALPHAL1 LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37
; CURRENT APPLICATION NUMBER: US/10/282,622
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/337,586
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1

```


LENGTH: 642
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (47) ... (532)
US-10-282-622-1

Query Match 74.0%; Score 299.6; DB 3; Length 642;
Best Local Similarity 84.1%; Pred. No. 2.9e-87;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 4 CAAGTCAAGATCCGACATGATTAGATGCGTCACTTATGATTTGATCAGCTG 63
DB 134 CAAGTCAAGATCCGACATGATTAGATGCGTCACTTATGATTTGATCAGCTG 193
QY 64 AAAAATTATGTAATGACCTGTTCCGGAATTCCTGCGGCTCCGGAAGATGTTGAGACC 123
DB 194 AAAAATTATGTAATGACCTGTTCCGGAATTCCTGCGGCTCCGGAAGATGTTGAGACC 253
QY 124 AACTGTAGTGTGCTGCTTTCTCTGTTTCCAGAAAGCCGCTGAAATCCGCAACACC 183
DB 254 AACTGTAGTGTGCTGCTTTCTCTGTTTCCAGAAAGCCGCTGAAATCCGCAACACC 313
QY 184 GGTAAACAAGACGATCATCAAGTTTCAATTAATAAAGTAAACGTAACCGCCGCTCC 243
DB 314 GGAACATGAAGATATCAATGATCAATTAATAAAGTAAACGTAACCGCCGCTCC 373
QY 244 ACCAAGCAGGTGCTGCTGACAAACACCGTCTGACCTGCTGATTTCTTATGAG 303
DB 374 ACAATGAGGAGGAAGACAGAAACAGACTTAACCTTCAATGATTTCTTATGAG 433
QY 304 AAAAATCCGCGGAAAGATTTCTGGAACGTTTCAATTCCTGCTGACAGAAATGATTAC 363
DB 434 AAAAATCCGCGGAAAGATTTCTGGAACGTTTCAATTCCTGCTGACAGAAATGATTAC 493
QY 364 CAGCAGCTGCTCTGCTGACCAAGTTCCGAAAGTTCTTCA 405
DB 494 CAGCAGCTGCTCTGCTGACCAAGTTCCGAAAGTTCTTCA 535

RESULT 9

US-09-825-561A-9
Sequence 9, Application US/09825561A
Patent No. 677539
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: No. 677539ak, Julia E.
APPLICANT: West, James W.
APPLICANT: Presnell, Scott R.
APPLICANT: Holly, Richard D.
APPLICANT: Nelson, Andrew J.
TITLE OF INVENTION: SOLUBLE ZALPHAL1 CYTOKINE RECEPTORS
FILE REFERENCE: 00-22
CURRENT APPLICATION NUMBER: US/09/825, 561A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/194,731
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/222,121
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 486
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1) ... (486)
US-09-825-561A-9

Query Match 73.2%; Score 296.6; DB 3; Length 486;
Best Local Similarity 84.0%; Pred. No. 2.4e-86;

Matches 335; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 4 CAAGTCAAGATCCGACATGATTAGATGCGTCACTTATGATTTGATCAGCTG 63
DB 88 CAAGTCAAGATCCGACATGATTAGATGCGTCACTTATGATTTGATCAGCTG 147
QY 64 AAAAATTATGTAATGACCTGTTCCGGAATTCCTGCGGCTCCGGAAGATGTTGAGACC 123
DB 148 AAAAATTATGTAATGACCTGTTCCGGAATTCCTGCGGCTCCGGAAGATGTTGAGACC 207
QY 124 AACTGTAGTGTGCTGCTTTCTCTGTTTCCAGAAAGCCGCTGAAATCCGCAACACC 183
DB 208 AACTGTAGTGTGCTGCTTTCTCTGTTTCCAGAAAGCCGCTGAAATCCGCAACACC 267
QY 184 GGTAAACAAGACGATCATCAAGTTTCAATTAATAAAGTAAACGTAACCGCCGCTCC 243
DB 268 GGAACATGAAGATATCAATGATCAATTAATAAAGTAAACGTAACCGCCGCTCC 327
QY 244 ACCAAGCAGGTGCTGCTGACAAACACCGTCTGACCTGCTGATTTCTTATGAG 303
DB 328 ACAATGAGGAGGAAGACAGAAACAGACTTAACCTTCAATGATTTCTTATGAG 387
QY 304 AAAAATCCGCGGAAAGATTTCTGGAACGTTTCAATTCCTGCTGACAGAAATGATTAC 363
DB 388 AAAAATCCGCGGAAAGATTTCTGGAACGTTTCAATTCCTGCTGACAGAAATGATTAC 447
QY 364 CAGCAGCTGCTCTGCTGACCAAGTTCCGAAAGTTCTTCA 402
DB 448 CAGCAGCTGCTCTGCTGACCAAGTTCCGAAAGTTCTTCA 486

RESULT 10

US-10-282-622-5
Sequence 5, Application US/10282622
Patent No. 6929932
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: No. 6929932ak, Julia E.
APPLICANT: West, James W.
TITLE OF INVENTION: ZALPHAL1 LIGAND ANTAGONISTS
FILE REFERENCE: 01-37
CURRENT APPLICATION NUMBER: US/10/282, 622
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 60/337,586
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 489
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: zalphal1 ligand Q153D/I156D
NAME/KEY: CDS
LOCATION: (1) ... (489)
US-10-282-622-5

Query Match 72.8%; Score 294.8; DB 3; Length 489;
Best Local Similarity 83.3%; Pred. No. 9.4e-86;
Matches 335; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 4 CAAGTCAAGATCCGACATGATTAGATGCGTCACTTATGATTTGATCAGCTG 63
DB 88 CAAGTCAAGATCCGACATGATTAGATGCGTCACTTATGATTTGATCAGCTG 147
QY 64 AAAAATTATGTAATGACCTGTTCCGGAATTCCTGCGGCTCCGGAAGATGTTGAGACC 123
DB 148 AAAAATTATGTAATGACCTGTTCCGGAATTCCTGCGGCTCCGGAAGATGTTGAGACC 207
QY 124 AACTGTAGTGTGCTGCTTTCTCTGTTTCCAGAAAGCCGCTGAAATCCGCAACACC 183
DB 208 AACTGTAGTGTGCTGCTTTCTCTGTTTCCAGAAAGCCGCTGAAATCCGCAACACC 267

```
QY 184 GGTAAACAAGATATCATCAAGTTTCCATTAAAGCTGAAGTAAACCGCGCTCC 243
Db 268 GAAAACATATAAGATAATCATATGATTAATAAGCTGAAGAGAAACACCTTCC 327
QY 244 ACCAAGCAGAGTGTCTGTGAGAAACACCGTCTGACCTGCCGTCTGTGATTTCTATGAG 303
Db 328 ACAATGCAAGGAGAAACAGAAACACAGACTAATCATGCCCTTATGTGATTTATGAG 387
QY 304 AAAAAACCGCGGAAAGATTCCTGGAACGTTCAATCCCTGCTGCAAAAATGATTCAC 363
Db 388 AAAAAACCGCAAGATTCCTGGAAGATTCGAAATCAATCACTTCTGATTAAGATGATCAT 447
QY 364 CAGCACTGTCTCTGTGACCAAGGTTCCGAAGATTCCTGA 405
Db 448 CAGCATGTCTCTGTGACCAAGGATTCCTGA 489
```

RESULT 11

```
US-09-522-217-84
; Sequence 84, Application US/09522217
; Patent No. 6307024
; GENERAL INFORMATION:
; APPLICANT: No. 6307024ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Foster, Cindy A.
; APPLICANT: Sprecher, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,547
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 84
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1560)
; OTHER INFORMATION: MBP-human zalpha11 ligand fusion polynucleotide
US-09-522-217-84
```

```
Query Match 72.5%; Score 293.6; DB 3; Length 1560;
Best Local Similarity 83.8%; Pred. No. 4.1e-85;
Matches 332; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
```

```
QY 10 CAAGATGCCACATGATTAGAAATGCGCAACTTATAGATATTTGTTAGTCAGCTGAATAAT 69
Db 1165 CAAGATGCCACATGATTAGAAATGCGCAACTTATAGATATTTGTTAGTCAGCTGAATAAT 1224
QY 70 TATGTGAATGACCTGTTCGGAATTCCTGCCGCTCCGGAAGATGTTGAGCAACTGT 129
Db 1225 TATGTGAATGACCTGTTCGGAATTCCTGCCGCTCCGGAAGATGTTGAGCAACTGT 1284
QY 130 GAGTGTCCGCTTTCTCTGTTTCCAGAAAGCCAGCTGAATTCGCAAAACACCGGTAC 189
Db 1285 GAGTGTCCGCTTTCTCTGTTTCCAGAAAGCCAGCTGAATTCGCAAAACACCGGTAC 1344
QY 190 AAGGAAGTATCATCAAGCTTTCCATTAAAAAATGAAAGCTAAACGCGGTCCACCAAC 249
Db 1345 AAGGAAGTATCATCAAGCTTTCCATTAAAAAATGAAAGCTAAACGCGGTCCACCAAC 249
```

```
Db 1345 AATGAAAGATATCATATGATTAATAAAGCTGAAGAGAAACACCTTCCAAAT 1404
QY 250 GCGTGTCTGTGAGAAACCGTGTGACCTGCCGCTGTGATTTTATGAGAAAAA 309
Db 1405 GCGAGGAGAGACAGAAACACAGACTAATGCCCTTATGATTTTATGAGAAAAA 1464
QY 310 CCGCCGAAAGATTCCTGGAAGATTCGAAATTCCTGCTGCAAAAATGATTCACAGCAC 369
Db 1465 CCAACCAAGATTTCTGAGAAATTCATTAATCACTTCCAAAAGATGATTCATGACAT 1524
QY 370 CTGTCTCTGTGACCAAGGTTCCGAAGATTCCTGA 405
Db 1525 CTGTCTCTGAGAACACAGAGGATTCCTGA 1560
```

RESULT 12

```
US-09-923-246-84
; Sequence 84, Application US/0923246
; Patent No. 6605272
; GENERAL INFORMATION:
; APPLICANT: No. 6605272ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; PRIOR FILING DATE: 2001-08-03
; EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 84
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1560)
; OTHER INFORMATION: MBP-human zalpha11 ligand fusion polynucleotide
US-09-923-246-84
```

```
Query Match 72.5%; Score 293.6; DB 3; Length 1560;
Best Local Similarity 83.8%; Pred. No. 4.1e-85;
Matches 332; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
```

```
QY 10 CAAGATGCCACATGATTAGAAATGCGCAACTTATAGATATTTGTTAGTCAGCTGAATAAT 69
Db 1165 CAAGATGCCACATGATTAGAAATGCGCAACTTATAGATATTTGTTAGTCAGCTGAATAAT 1224
QY 70 TATGTGAATGACCTGTTCGGAATTCCTGCCGCTCCGGAAGATGTTGAGCAACTGT 129
Db 1225 TATGTGAATGACCTGTTCGGAATTCCTGCCGCTCCGGAAGATGTTGAGCAACTGT 1284
QY 130 GAGTGTCCGCTTTCTCTGTTTCCAGAAAGCCAGCTGAATTCGCAAAACACCGGTAC 189
Db 1285 GAGTGTCCGCTTTCTCTGTTTCCAGAAAGCCAGCTGAATTCGCAAAACACCGGTAC 1344
QY 190 AAGGAAGTATCATCAAGCTTTCCATTAAAAAATGAAAGCTAAACGCGGTCCACCAAC 249
Db 1345 AAGGAAGTATCATCAAGCTTTCCATTAAAAAATGAAAGCTAAACGCGGTCCACCAAC 249
QY 250 GCGTGTCTGTGAGAACACAGAGGATTCCTGA 1560
Db 1525 GCGTGTCTGTGAGAACACAGAGGATTCCTGA 1560
```

Db 1405 GCAGGAGAGACAGAAACACAGACTAACATGCCCTTCTGATGATTTTATGAGAAAAA 1464
Qy 310 CCGCCGAAAGATTCTTGAAACGTTTCAATCCCTGCTGCAGAAAAATGATTCACGAGC 369
Db 1465 CCACCAAGAAATTCCTTGAAGAAATTCATCACTTCTCCAAAGATGATTCATGAGCAT 1524
Qy 370 CTGTCTCTCTGTAACCAAGGTTCCGAAGATTCCTGA 405
Db 1525 CTGTCTCTAGAAACACAGGAGTGAAGATTCCTGA 1560

RESULT 13
US-10-295-723-84
Sequence 84, Application US/10295723
Patent No. 6686178

GENERAL INFORMATION:
APPLICANT: No. 6686178ak, Julia E.
APPLICANT: Priesnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA1 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/10/295,723
PRIOR FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: 09/522,217
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/123,547
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 84
LENGTH: 1560
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1560)
OTHER INFORMATION: MBP-human zalpha1 ligand fusion polynucleotide
US-10-295-723-84

Query Match 72.5% Score 293.6; DB 3; Length 1560;
Best Local Similarity 83.8%; Pred. No. 4.1e-85;
Matches 332; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 10 CAAGATCCCAATGATAGATGCGTCACTTATAGATATGTTGATCAGCTGAAAAAT 69
Db 1165 CAAGATCCCAATGATAGATGCGTCACTTATAGATATGTTGATCAGCTGAAAAAT 1224
Qy 70 TATGTGATGACCTGTGTCGGAATTCCTGCGGCTCCGGAAGATGTGAGACCAACTGT 129
Db 1225 TATGTGATGACCTGTGTCGGAATTCCTGCGGCTCCGGAAGATGTGAGACCAACTGT 1284
Qy 130 GAGTGTCCGCTTCTCGGTTTCAGAAAGCCAGCTGAATCCGCAAAACACCGGTATC 189
Db 1285 GAGTGTCCGCTTCTCGGTTTCAGAAAGCCAGCTGAATCCGCAAAATCAGAGAAC 1344
Qy 190 AACGAACGTATCATCAAGTTTCAATTAATACTGAACGTAACCGCGCTCACCAAC 249
Db 1345 AATGAACGTATCATCAATGTATCAATTAATAAGTGAAGAGAACCACTTCCCAAAAT 1404
Qy 250 GCAGTGTCTGTGAGAAACACCGGTGACCTGCGCTGTGATTTTATGAGAAAAA 309

Db 1405 GCAGGAGAGACAGAAACACAGACTAACATGCCCTTCTGATGATTTTATGAGAAAAA 1464
Qy 310 CCGCCGAAAGATTCTTGAAACGTTTCAATCCCTGCTGCAGAAAAATGATTCACGAGC 369
Db 1465 CCACCAAGAAATTCCTTGAAGAAATTCATCACTTCTCCAAAGATGATTCATGAGCAT 1524
Qy 370 CTGTCTCTCTGTAACCAAGGTTCCGAAGATTCCTGA 405
Db 1525 CTGTCTCTAGAAACACAGGAGTGAAGATTCCTGA 1560

RESULT 14
US-09-522-217-3
Sequence 3, Application US/09522217
Patent No. 6307024

GENERAL INFORMATION:
APPLICANT: No. 6307024ak, Julia E.
APPLICANT: Priesnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA1 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/522,217
PRIOR FILING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: US 60/142,013
EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 486
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Degenerate polynucleotide sequence for human
OTHER INFORMATION: zalpha1 ligand
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(486)
OTHER INFORMATION: n = A,T,C or G
US-09-522-217-3

Query Match 71.8% Score 290.6; DB 3; Length 486;
Best Local Similarity 56.5%; Pred. No. 2.2e-84;
Matches 225; Conservative 114; Mismatches 59; Indels 0; Gaps 0;

Qy 4 CAAGTCAAGATCCGACATGATTAAGATGCGTCACTTATAGATATGTTGATCAGCTG 63
Db 88 CAGGNCARGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 147
Qy 64 AAAAATTTGTGATGACCTGTGTCGGAATTCCTGCGGCTCCGGAAGATGTGAGACC 123
Db 148 AAAAATTTGTGATGACCTGTGTCGGAATTCCTGCGGCTCCGGAAGATGTGAGACC 207
Qy 124 AACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 183
Db 208 AACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 267
Qy 184 GGTAAACGAACGTATCATCAAGTTTCAATTAATACTGAACGTAACCGCGCTCC 243
Db 268 GGTAAACGAACGTATCATCAAGTTTCAATTAATACTGAACGTAACCGCGCTCC 327
Qy 244 ACCAAGCAGTGTGTCGAGAAACACCGGTGACCTGCGCTGTGATTTTATGAG 303

Db 328 ACNAAVCGNGMNGMNCARCAARCAVWNTYNACTGTCNMSNTGAYWSTAYGAR 387
Qy 304 AAAAAGCGCGAAGAAATTCCTGGAACGTTTCAATCCCTGCTGACGAAAATGATTAC 363
Db 388 AARARCCNCCNAAARGARTTYTNGARMGNTTYAARWNTYNTYNCARAAATGATTCAY 447
Qy 364 CAGCACTGTCCTCTGCTACCCACGCTTCCGAAATTC 401
Db 448 CARCAYYTNWMSNMGNACNCAVGNMWSNGARGAYWS 485

RESULT 15
US-09-923-246-3
; Sequence 3, Application US/09923246
; Patent No. 6605272
; GENERAL INFORMATION:
; APPLICANT: No. 6605272ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923, 246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522, 217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 486
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Degenerate polynucleotide sequence for human
; NAME/KEY: misc_feature
; LOCATION: (1)..(486)
; OTHER INFORMATION: n = A,T,C or G
US-09-923-246-3

Query Match 71.8%; Score 290.6; DB 3; Length 486;
Best Local Similarity 56.5%; Pred. No. 2.2e-84;
Matches 225; Conservative 114; Mismatches 59; Indels 0; Gaps 0;

Qy 4 CAAGGTCAAGATCCGACATGATAGATGCGTCACTTATGATGTTGATCAGCTG 63
Db 88 CARGNCARGAYMNCAYATGATMGNAATGNCARATYNATHGAYATHGTGACARATN 147
Qy 64 AAAAATTATGTGAATGACCTGCTGCGAATTCCTGCGGCTCCGAAAGATGTTGAGACC 123
Db 148 AARAAATYATGTAAGAYTGTGTCNCNGARTTYTTCNCGNCNGARGAGATGARGACN 207
Qy 124 AACGTGAGTGGTCCGCTTCTCTGTTTCCAGAAAGCCGAGCTGAATCCGCAACACC 183
Db 208 AAYTGYARTGWSNGNTTYWSNTGYTTCARARAGCNCARATYNAAWWSNGNAAYACN 267
Qy 184 GGTAAACAGCAACGTATCATCAAGTTTCAATTAATAAATGAACGTAACCCGCTCC 243
Db 268 GGNAAVAYAYGARMGNAHTAHTAAAGTWSNATHAARARATYNAAARMGNAARCCNWSN 327
Qy 244 ACCAAGCAGCTGCTGCTGACGAAACACCGTGAACCTGCTGCTGATTTATGAG 303
Db 328 ACNAAVCGNGMNGMNCARCAARCAVWNTYNACTGTCNMSNTGAYWSTAYGAR 387

Qy 304 AAAAAGCGCGAAGAAATTCCTGGAACGTTTCAATCCCTGCTGACGAAAATGATTAC 363
Db 388 AARARCCNCCNAAARGARTTYTNGARMGNTTYAARWNTYNTYNCARAAATGATTCAY 447
Qy 364 CAGCACTGTCCTCTGCTACCCACGCTTCCGAAATTC 401
Db 448 CARCAYYTNWMSNMGNACNCAVGNMWSNGARGAYWS 485

Search completed: August 7, 2006, 12:12:48
Job time : 151 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2006, 12:13:07 ; Search time 1011 Seconds
(without alignments)
4922.346 Million cell updates/sec

Title: US-10-735-149-27

Perfect score: 405

Sequence: 1 atgaaggtcgaagatcgcca.....acggtccgaagattcctga 405

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11E_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	299.6	74.0	483	US-09-923-246-63	Sequence 63, Appl
2	299.6	74.0	483	US-10-295-723-63	Sequence 63, Appl
3	299.6	74.0	483	US-10-659-684-63	Sequence 63, Appl
4	299.6	74.0	483	US-10-787-442-63	Sequence 63, Appl
5	299.6	74.0	489	US-10-775-204-2157	Sequence 2157, Ap
6	299.6	74.0	642	US-09-923-246-1	Sequence 1, Appl
7	299.6	74.0	642	US-10-295-723-1	Sequence 1, Appl
8	299.6	74.0	642	US-10-282-622-1	Sequence 1, Appl
9	299.6	74.0	642	US-10-456-780-1	Sequence 1, Appl
10	299.6	74.0	642	US-10-659-684-1	Sequence 1, Appl
11	299.6	74.0	642	US-10-787-442-1	Sequence 1, Appl
12	299.6	74.0	642	US-10-951-239-1	Sequence 1, Appl
13	299.6	74.0	642	US-11-174-398-1	Sequence 1, Appl
14	299.6	74.0	642	US-11-134-489-1	Sequence 1, Appl
15	298	73.6	611	US-11-137-807-11	Sequence 11, Appl
16	298	73.6	617	US-09-972-218A-18	Sequence 18, Appl
17	298	73.6	617	US-10-264-634-18	Sequence 18, Appl

18	298	73.6	617	US-10-620-169-1	Sequence 1, Appl
19	298	73.6	617	US-11-132-947-1	Sequence 1, Appl
20	298	73.6	617	US-11-187-488-18	Sequence 18, Appl
21	296.6	73.2	399	US-10-867-992-18	Sequence 9, Appl
22	296.6	73.2	486	US-09-825-561A-9	Sequence 9, Appl
23	296.6	73.2	486	US-10-872-087-9	Sequence 9, Appl
24	294.8	72.8	489	US-10-282-622-5	Sequence 5, Appl
25	294.8	72.8	489	US-11-174-398-5	Sequence 5, Appl
26	293.6	72.5	1560	US-09-923-246-84	Sequence 84, Appl
27	293.6	72.5	1560	US-10-295-723-84	Sequence 84, Appl
28	293.6	72.5	1560	US-10-659-684-84	Sequence 84, Appl
29	293.6	72.5	1560	US-10-787-442-84	Sequence 84, Appl
30	290.6	71.8	486	US-09-923-246-3	Sequence 3, Appl
31	290.6	71.8	486	US-10-295-723-3	Sequence 3, Appl
32	290.6	71.8	486	US-10-659-684-3	Sequence 3, Appl
33	290.6	71.8	486	US-10-787-442-3	Sequence 3, Appl
34	264.4	65.3	444	US-10-282-622-3	Sequence 3, Appl
35	264.4	65.3	444	US-11-174-398-3	Sequence 3, Appl
36	261.4	64.5	399	US-10-867-992-11	Sequence 11, Appl
37	259.8	64.1	399	US-10-867-992-13	Sequence 13, Appl
38	256	63.2	393	US-10-867-992-3	Sequence 3, Appl
39	256	63.2	393	US-10-867-992-9	Sequence 9, Appl
40	254.4	62.8	393	US-10-867-992-5	Sequence 5, Appl
41	254.4	62.8	393	US-10-867-992-7	Sequence 7, Appl
42	252.8	62.4	393	US-10-867-992-1	Sequence 1, Appl
43	182	44.9	3072	US-09-923-246-55	Sequence 55, Appl
44	182	44.9	3072	US-09-825-561A-46	Sequence 46, Appl
45	182	44.9	3072	US-10-295-723-55	Sequence 55, Appl

ALIGNMENTS

RESULT 1
US-09-923-246-63
Sequence 63, Application US/09923246

Patent No. US20020128446A1

GENERAL INFORMATION:

APPLICANT: No. US20020128446A1ak, Julia E.

APPLICANT: Presnell, Scott R.

APPLICANT: Sprecher, Cindy A.

APPLICANT: Poester, Donald C.

APPLICANT: Holly, Richard D.

APPLICANT: Gross, Jane A.

APPLICANT: Johnston, Janet V.

APPLICANT: Nelson, Andrew J.

APPLICANT: Dillon, Stacey R.

APPLICANT: Hammond, Angela K.

TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND

FILE REFERENCE: 99-16

CURRENT APPLICATION NUMBER: US/09/923,246

PRIOR FILING DATE: 2001-08-03

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217

PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09

PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-03-11

PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US 60/142,013

NUMBER OF SEQ ID NOS: 115

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 63

LENGTH: 483

TYPE: DNA

ORGANISM: homo sapiens

US-09-923-246-63

Query Match

Best local similarity 84.1%; Pred. No. 1,56-87;

Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Cy 4 CAAGTCAAGTTCGCCACATGATTGAGATGGCTCAACTATGATGTTGATCAGCTG 63

Db 82 CAAGTCAAGTTCGCCACATGATTGAGATGGCTCAACTATGATGATTGATCAGCTG 141

Qy	6	AAAAATTATGTGAATGACCGGGTCCGGAAATTCGCGCGGGCTCGGAAAGATGTTGAAC	123
Db	142	AAAAATTATGTGAATGACCTGGTCCCTGAATTTCTGCGAGCTCCGAAAGATGTGAAC	201
Qy	124	AACGTGAGTGATCGCGTTTCTCTGTGTTCCGAAAGCCGACTGAAATCGCAACACC	183
Db	202	AACGTGAGTGATCGAGCTTTTCTGTTTTCAGAAAGGCCCAACTAAAGTCGCAAAATCA	261
Qy	184	GGTACACGACGATCATCAACGTTTCCATTTAAATAACGTAAACGTAAACCGCGTCC	243
Db	262	GGAAACATATGAATGATATCATGATATCAATTTAAAGCTGAAGAGAAACACCTTCC	321
Qy	244	ACCAAGCGAGGTCTGCTGAGAAACACCGTCTGACCTGCGGTCTGTGATTTCTTAAG	303
Db	322	ACAAATGCAAGGAGGAAGACAGAAACACACTCAATCATCCCTTCAATGATTTCTTAAG	381
Qy	304	AAAAAACCGCCGAANAATTCCTGGAACGTTCAATCTCTGCTGACGAAAGATGATTCAC	363
Db	382	AAAAAACCAACCAAAATTTCTGAAGAAATTTCAATCACTTCTCCAAAGATGATTCAT	441
Qy	364	CAGCAGCTGTCTCTCTGTAACCAAGGTTCCGAAGATTCCTGA	405
Db	442	CAGCATCTGTCTCTTGAACCAACGGAAGTGAAGATTCCTGA	483

```

RESULT 2
US-10-295-723-63
Sequence 63, Application US/10295723
Publication No. US20030125524A1
GENERAL INFORMATION:
APPLICANT: No. US20030125524A1ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/10/295,723
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: 09/522,217
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/123,547
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 63
LENGTH: 483
TYPE: DNA
ORGANISM: homo sapiens
US-10-295-723-63

```

[illegible]

QY	184	GGTAAACAAGCAAGTATCATCAAGCTTTCCATTAAAAA	CTGAACGTAACCGCCGCTC	243
QY <td>124</td> <td>TAAGTGAAGTGTGCGACTTTCTCTGTTTCCAGAAGCCCACTGTAATCCCAACACC</td> <td></td> <td>183</td>	124	TAAGTGAAGTGTGCGACTTTCTCTGTTTCCAGAAGCCCACTGTAATCCCAACACC		183
Db	202	AAGTGTAGTGTGAGCTTTTCTCTGTTTTCAGAAAGGCCCACTAAAGTCAGAAATACA		261
QY <td>184</td> <td>GGTAAACAAGCAAGTATCATCAAGCTTTCCATTAAAAA<td>CTGAACGTAACCGCCGCTC</td><td>243</td></td>	184	GGTAAACAAGCAAGTATCATCAAGCTTTCCATTAAAAA <td>CTGAACGTAACCGCCGCTC</td> <td>243</td>	CTGAACGTAACCGCCGCTC	243
Db	262	GGAAACATGAAAGATATCATGATTAACAATTAATAAAGCTGACAGGAAACCACTTCC		321
QY <td>244</td> <td>ACCAACGAGGTCGTGCTCAGAAAACCGCTGCACTGCGCTCGTATTTCTATGAG</td> <td></td> <td>303</td>	244	ACCAACGAGGTCGTGCTCAGAAAACCGCTGCACTGCGCTCGTATTTCTATGAG		303
Db	322	ACAAATGCAAGGAGAAACAGAAACACAGACTTAACATGCCCTTCATGTGATTTCTATGAG		381
QY <td>304</td> <td>AAAAAACCGCGAAGAAATTCCTGGAACGTTCAATCCCTGCTGCAGAAAATGATTCA</td> <td></td> <td>363</td>	304	AAAAAACCGCGAAGAAATTCCTGGAACGTTCAATCCCTGCTGCAGAAAATGATTCA		363
Db	382	AAAAAACCAACCAAGAAATTCCTGAAGAAATTCATCAATCACTTCTCCAAAAAGATGATTCA		441
QY <td>364</td> <td>CAGCACTGTCTCTCTGTAACCAAGAGTTCCGAAGATTCCTGA</td> <td></td> <td>405</td>	364	CAGCACTGTCTCTCTGTAACCAAGAGTTCCGAAGATTCCTGA		405
Db	442	CAGCATCTGTCTCTAGAACACAGGAAGTGAAGATTCCTGA		483

```

RESULT 3      US-10-659-684-63
; Sequence 63, Application US/10659684
; Publication No. US20040110932A1
; GENERAL INFORMATION:
; APPLICANT: Novak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/659,684
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 483
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-659-684-63

```

Query Match	74.0%	Score 299.6	DB 8	Length 483
Best Local Similarity	84.1%	Pred. No. 1.5e-87		
Matches 338	Conservative 0	Mismatches 64	Indels 0	Gaps 0

QY	4	CAAGTCAMATGCGCCACATATAGAAATGCGTCAACTTATAGATATATTGTTGATCAAGCTG	63
Db	82	CAAGTCAMAGATGCGCACATATAGATAGATGCGTCAACTTATAGATATATTGTTGATCAAGCTG	141

QY	64	AAAAATTATGGAATGACCTGCTGTTCCGGAAATTCCTGCGCGGTCCGGAAAGATGTGAACC	123
Db	142	AAAAATTATGGAATGACTGGTCTCCGTGAATTTCTGCAAGTCCAGAAAGATGTAAGCA	201

QY	124	AACTGTAGTGTGTCGCTTTCTCCTGTTTCCAGAAAGCCAGCTGAATCCGCAAAACCC	183
Db	202	AACTGTAGTGTGTCAGCTTTTCTGTTTTCAGAAAGGCCCAACTAAAGTCAAGCAAAATCA	261

QY	184	GGTACACACGAGCATATCATCAAGTTTCCATTAAAACTGAAAGCTAAACCGCGCTCC	243
----	-----	---	-----

```
Db 262 GGAACCAATGAAAGATATATCAATGATTAATAAGATGAGGAAACACCTTCC 321
Qy 244 ACCAACGCGAGGTGCTGTGTAAGAAACCGCTCTGACCTGCCGCTGTGATTTATGAG 303
Db 322 ACAAATGCGAGGAGAGAGACAAACACACTTAACATGCGCTTCATGATTTCTTATGAG 381
Qy 304 AAAAAACCGCGAAAGAAATTCCTGTGAAGCTTCAATTCCTGTGAGAAATGATTCAC 363
Db 382 AAAAAACCGCGAAAGAAATTCCTGTGAAGATTCATTAATTCCTGTGAGAAATGATTCAT 441
Qy 364 CAGCACTGTCTCTCTGTACCCAGCGTTCGAAATTCCTGA 405
Db 442 CAGCATCTGTCTCTGTAGAACACAGCAAGTGAAGATTCCTGA 483

RESULT 4
US-10-787-442-63
; Sequence 63, Application US/10787442
; Publication No. US20040260065A1
; GENERAL INFORMATION:
; APPLICANT: Novak, Julia E.
; APPLICANT: Preenell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAN1 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/787,442
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 483
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-787-442-63

Query Match 74.0%; Score 299.6; DB 9; Length 483;
Best Local Similarity 84.1%; Pred. No. 1.5e-87;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 4 CAAGTCAAGATCGCCACATGATTAAGATGCGTCAACTTAATGATTTGATGAGCTG 63
Db 82 CAAGTCAAGATCGCCACATGATTAAGATGCGTCAACTTAATGATTTGATGAGCTG 141
Qy 64 AAAAAATTGTAAGATGACCTGTTCCGGAATTCGCGCGCTCCGGAAGATTTGAGACC 123
Db 142 AAAAAATTGTAAGATGACCTGTTCCGGAATTCGCGCGCTCCGGAAGATTTGAGACA 201
Qy 124 AACTGTGAGTGTCCGCTTTCTCTGTTTCCAGAAAGCCAGCTGAAATCCGCAACACC 183
Db 202 AACTGTGAGTGTGACGCTTTTCTCTGTTTCCAGAAAGCCAGCTGAAATCCGCAACACC 261
Qy 184 GGTAAACAAGACGATCATCAAGCTTTCCATTAATAAACTGAAAAGTAAACCGCGCTCC 243
Db 262 GGAACAATGAAAGATATCAATGATTAATAAAAGCTGAAAGGAAACCACTTCC 321
Qy 244 ACCAAGAGGTGCTGTGAGAAACAGCTGAGCTGCCCTCTGTGATTTCTATGAG 303
```

```
Db 322 ACAAATGCGAGGAGAGACAGAAACACAGACTAATGCGCTTCATGATTTCTATGAG 381
Qy 304 AAAAAACCGCGAAAGAAATTCCTGTGAAGCTTCAATTCCTGTGAGAAATGATTCAC 363
Db 382 AAAAAACCGCGAAAGAAATTCCTGTGAAGATTCATTAATTCCTGTGAGAAATGATTCAT 441
Qy 364 CAGCACTGTCTCTCTGTACCCAGCGTTCGAAATTCCTGA 405
Db 442 CAGCATCTGTCTCTGTAGAACACAGCAAGTGAAGATTCCTGA 483

RESULT 5
US-10-775-204-2157
; Sequence 2157, Application US/10775204
; Publication No. US20050186664A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Haseltine, William A.
; APPLICANT: Balance, David J.
; APPLICANT: Turner, Andrew J.
; TITLE OF INVENTION: Alduin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/10/775,204
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 60/423,623
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/351,360
; PRIOR FILING DATE: 2002-01-28
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2157
; LENGTH: 489
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-204-2157

Query Match 74.0%; Score 299.6; DB 10; Length 489;
Best Local Similarity 84.1%; Pred. No. 1.5e-87;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 4 CAAGTCAAGATCGCCACATGATTAAGATGCGTCAACTTAATGATTTGATGAGCTG 63
Db 88 CAAGTCAAGATCGCCACATGATTAAGATGCGTCAACTTAATGATTTGATGAGCTG 147
Qy 64 AAAAAATTGTAAGATGACCTGTTCCGGAATTCGCGCGCTCCGGAAGATTTGAGACC 123
Db 148 AAAAAATTGTAAGATGACCTGTTCCGGAATTCGCGCGCTCCGGAAGATTTGAGACA 207
Qy 124 AACTGTGAGTGTCCGCTTTCTCTGTTTCCAGAAAGCCAGCTGAAATCCGCAACACC 183
Db 208 AACTGTGAGTGTGACGCTTTTCTCTGTTTCCAGAAAGCCAGCTGAAATCCGCAACACC 267
Qy 184 GGTAAACAAGACGATCATCAAGCTTTCCATTAATAAACTGAAAAGTAAACCGCGCTCC 243
Db 268 GGAACAATGAAAGATATCAATGATTAATAAAAGCTGAAAGGAAACCACTTCC 327
```


QY	24	328	304	388	364	448
QY	ACCAAGCAGGTGTGTGTAGAAACCGTGCAGCTCCGTCTGTGATTTCTTAGAG	ACAAATGCAGAGGAGGAAGAAACACACACTTACATGCCCTTCATGTGATTTCTTAGAG	AAAAAACCGCGGAAGAATTTCCTCGGAAGTTTCAATCCCTGTCAGAAAAATGATTCAC	AAAAAACCCACCAAGAAATTTCTGAGAAAGATTCAATCATCTTCCAAAAAGATATTCAT	CAGCACTGTCTCTCTGTACACGGTTTCCGAAGATTCCTGA	CAGCATTTGTCTCTTAGAACACACGGAAGTAGAATTCCTGA
Db						
QY						
Db						

RESULT 6

```

US-09-923-246-1
Sequence 1, Application US/09923246
Patent No. US20020128446A1
GENERAL INFORMATION:
APPLICANT: No. US20020128446A1aK, Julia E.
APPLICANT: Prenselli, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/923.246
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 642
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (47)...(532)
US-09-923-246-1

```

Query Match	74.0%;	Score 299.6;	DB 3;	Length 642;
Best Local Similarity	84.1%;	Pred. No. 1.7e-87;		
Matches 338;	Conservative 0;	Mismatches 64;	Indels 0;	Gaps 0;

[illegible]

QY 304 AAAAAACGGCGAAGAAATTTCTGGAAAGTTTCAATCCCTGTCGAGAGAAATGATTCAC 363
434 AAAAAACCAACCGAAGAAATTTCTAGAAAGATTCMAATCACTTCTCCAAAAAGATGATTCAT 493

Db

QY 364 CAGCACCTGTCTCTCTGTAACCAAGGTTCCGAAAGTTCTCTGA 405

Db 494 CAGCATCTGTCTCTTAGAACAACACGGAAGTGAAGATTCCTGA 535

RESULT 7

```

US-10-295-723-1
; Sequence 1, Application US/10295723
; Publication No. US20030125524A1
GENERAL INFORMATION:
; APPLICANT: No. US20030125524A1ak, Julia E.
; APPLICANT: Preenell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND
FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo sapiens
FEATURE:
; NAME/KEY: CDS
; LOCATION: (47)...(532)
US-10-295-723-1

```

Query Match	74.0%;	Score 299.6;	DB 7;	Length 642;
Best Local Similarity	84.1%;	Pred. No. 1.7e-87;		
Matches 338;	Conservative 0;	Mismatches 64;	Indels 0;	Gaps 0;

Oy 4 CAAGTCGAAGATCGGCACATGATTGAAATGCGTCAACTATATGATTTGTTATCAGCTG 63
 Db 134 CAAGGTCAAGATCGGCACATGATTGAAATGCGTCAACTATATGATTTGTTATCAGCTG 193
 Oy 64 AAAAATTATGTGAATGACCTGGTCCGGAATTCCTGCCGCTCCGGAGATGTTTGAGACC 123
 Db 194 AAAATTATGTGAATGACCTGGTCCGGAATTCCTGCCGCTCCGGAGATGTTTGAGAGACA 253
 Oy 124 AACTGTGATGGTCCGCTTTCTCTGTTTCCAGAAAGCCGACGTGAATTCGCGAAACACC 183
 Db 254 AACTGTGATGGTCAAGCTTTTCTCTGTTTCCAGAAAGCCGCACTAAAGTCAGCAAAATACA 313
 Oy 184 GGTAAACAACGACGATATCAACGTTTCCATTAAAAAACGTGAAGGTAAACCGCGCTCC 243
 Db 314 GGAACCAATGAAGGATATATCATGTATTAATTAATAAACCTGAAGAGAAACCACTTCC 373
 Oy 244 ACCAACGAGGCTGTCTGCAGAAACACGCTGACCTGCCGCTCTGTGATTTCTTATGAG 303
 Db 374 ACAATATCGAGGAGAAAGACAGAAACACGACTATACATGCCCTTCATGTGATTTCTTATGAG 433
 Oy 304 AAAAAACGCGAANAAGAAATTCCTGGAACGTTTCAATCCCTGTGCAAGAAATGATTCAC 363

Db 434 AAAAAACCAACCAAGAAATTCCTAGAAAGATTCACATCTTCCAAAAGATGATCAT 493
Qy 364 CAGACCTGTCTCTCCGTACCAACCGTCCGAAAGTTCTCTGA 405
Db 494 CAGCATCTGTCTCTTAGAACAACGGAAGTGAAGATTCCTGA 535

RESULT 8

US-10-282-622-1
; Sequence 1, Application US/10282622
; Publication No. US20030134390A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: West, James W.
; APPLICANT: NO. US20030134390A1ak, Julia E.
; TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37
; CURRENT APPLICATION NUMBER: US/10/282,622
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/337,586
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (47) ... (532)
US-10-282-622-1

Query Match 74.0%; Score 299.6; DB 7; Length 642;

Best Local Similarity 84.1%; Pred. No. 1.7e-87;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 4 CAAGTCAAGATCCGACATGATTAGATGCGTCACTTATAGATTTGATGATGCTG 63
Db 134 CAAGTCAAGATCCGACATGATTAGATGCGTCACTTATAGATTTGATGATGCTG 193
Qy 64 AAAAAATTATGTGAATGACCTGTGCTCCGGAATTCCTGCGGCTCCGGAAGATTTGAGACC 123
Db 194 AAAAAATTATGTGAATGACCTGTGCTCCGGAATTCCTGCGGCTCCGGAAGATTTGAGACA 253
Qy 124 AACTGTGAGTGTCGCTTCTTCTCTGTTTCCAGAAAGCCAGCTGAAATCCGCAAAACC 183
Db 254 AACTGTGAGTGTCGCTTCTTCTGTTTCCAGAAAGCCAGCTGAAATCCGCAAAATACA 313
Qy 184 GGTAAACAAGACGATATCATGACGTTTCCATTTAAAAAAGCTGAAACGTAACCGCGCTCC 243
Db 314 GGAACAATGAAAGATATCATGATATCAATTTAAAAAGCTGAAAGAGAAACCACTTCC 373
Qy 244 ACCAAGCAGGTCGTCGTCAAGAAACACCGTGCACCTGCGTCTGATTTCTATGAG 303
Db 374 ACAATGCAAGGAGAGACAGAAACACAGACTACATCCCTTCACTGATTTCTTATGAG 433
Qy 304 AAAAAACCGCCGAAAGAAATTCCTGGAACGTTTCAATCCCTGCTGCAGAAAAATGATTCAC 363
Db 434 AAAAAACCGCCGAAAGAAATTCCTGGAAGATTTCAATCACTTCTCAAAAGATGATTCAT 493
Qy 364 CAGACCTGTCTCTCTGTAACCAACGCTTCCGAAAGTTCTCTGA 405
Db 494 CAGCATCTGTCTCTTAGAACAACGGAAGTGAAGATTCCTGA 535

RESULT 9

US-10-456-780-1
; Sequence 1, Application US/10456780
; Publication No. US20040009150A1
; GENERAL INFORMATION:
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Hughes, Steven D.
; APPLICANT: Holly, Richard D.

; TITLE OF INVENTION: USE OF IL-21 IN CANCER AND
; TITLE OF INVENTION: OTHER THERAPEUTIC APPLICATIONS
; FILE REFERENCE: 03-08
; CURRENT APPLICATION NUMBER: US/10/456,780
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/387,127
; PRIOR FILING DATE: 2002-06-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (47) ... (532)
US-10-456-780-1

Query Match 74.0%; Score 299.6; DB 7; Length 642;

Best Local Similarity 84.1%; Pred. No. 1.7e-87;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 4 CAAGTCAAGATCCGACATGATTAGATGCGTCACTTATAGATTTGATGATGCTG 63
Db 134 CAAGTCAAGATCCGACATGATTAGATGCGTCACTTATAGATTTGATGATGCTG 193
Qy 64 AAAAAATTATGTGAATGACCTGTGCTCCGGAATTCCTGCGGCTCCGGAAGATTTGAGACC 123
Db 194 AAAAAATTATGTGAATGACCTGTGCTCCGGAATTCCTGCGGCTCCGGAAGATTTGAGACA 253
Qy 124 AACTGTGAGTGTCGCTTCTTCTCTGTTTCCAGAAAGCCAGCTGAAATCCGCAAAACC 183
Db 254 AACTGTGAGTGTCGCTTCTTCTGTTTCCAGAAAGCCAGCTGAAATCCGCAAAATACA 313
Qy 184 GGTAAACAAGACGATATCATGACGTTTCCATTTAAAAAAGCTGAAACGTAACCGCGCTCC 243
Db 314 GGAACAATGAAAGATATCATGATATCAATTTAAAAAGCTGAAAGAGAAACCACTTCC 373
Qy 244 ACCAAGCAGGTCGTCGTCAAGAAACACCGTGCACCTGCGTCTGATTTCTTATGAG 303
Db 374 ACAATGCAAGGAGAGACAGAAACACAGACTACATCCCTTCACTGATTTCTTATGAG 433
Qy 304 AAAAAACCGCCGAAAGAAATTCCTGGAACGTTTCAATCCCTGCTGCAGAAAAATGATTCAC 363
Db 434 AAAAAACCGCCGAAAGAAATTCCTGGAAGATTTCAATCACTTCTCAAAAGATGATTCAT 493
Qy 364 CAGACCTGTCTCTCTGTAACCAACGCTTCCGAAAGTTCTCTGA 405
Db 494 CAGCATCTGTCTCTTAGAACAACGGAAGTGAAGATTCCTGA 535

RESULT 10

US-10-659-684-1
; Sequence 1, Application US/10659684
; Publication No. US20040110932A1
; GENERAL INFORMATION:
; APPLICANT: Novak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprenger, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Nelson, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/659,684
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,547

```

? PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09      US 60/123,904
? PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
? PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
? PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
? PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
? NUMBER OF SEQ ID NOS: 115
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 1
? LENGTH: 642
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (47)...(532)
? US-10-659-684-1

```

Query Match	74.0%	Score 299.6	DB 8	Length 642
Best Local Similarity	84.1%	Pred. No. 1.7e-87		
Matches 338	Conservative 0	Mismatches 64	Indels 0	Gaps 0

QY	4	CAAGGTCAGATGCGCACATGATTGAAATGACGTCAACTTAATAGATAATGTTGATCAACTG	63
Db	134	CAAGGTCAGATGCGCACATGATTGAAATGAAATGCGTCAACTTAATGATATTGTTGATCAACTG	139
QY	64	AAAAATTAATGTGATGATGACCTGTGTCGGAAATTCCTGCGGGCTCCGGAAAGATGTTGAGACC	123
Db	194	AAAAATTAATGTGATGATGACCTGTGTCGGAAATTCCTGCGAGCTCCGAAAGATGTTGAGACA	253
QY	124	AACCTGAGAGTGTCCGCTTTCTTCCTGTTTCCAGAAAGCCGAGCTGAAATCCGCAAAACCC	183
Db	254	AACCTGAGAGTGTCCGACTTTTCTCTGTTTTCAGAAAGGCCCAACTAACTGACAAATACA	313
QY	184	GGTACACACGACGTATCATCAACGTTTCCATTAAAACTGAAACGTAAACCGCCGCTCC	243
Db	314	GGAAACATATGAAGATTAATCAATGATATCAATTAATAAAACTGAAAGAAACCACTTCC	373
QY	244	ACCAACGACAGTGTGCTGACGAAACAACGCTCTGACCTGCGCTCTGATTTCTTATGAG	303
Db	374	ACAAATGACGAGGAGAAACAGAAACAACAATCAATGCGCTTATGATTTCTTATGAG	433
QY	304	AAAAAACCGCCGAAAGAAATTTCTGGAACGTTTCAATCCCTGCTGCAGAAAAATGATTAC	363
Db	434	AAAAAACCAACCCAAAGAAATTTCTGAGAAAGATTCAAATCACTTCTCCAAAGATGATTCAT	493
QY	364	CAGACCTGTCTCTGTGTAACCAAGGTTCCGAAGATTCCTGA	405
Db	494	CAGCATCTGTCTCTTAGAAACAACGGAATGAAAGATTCCTGA	535

```

1 RESULT 11
2 US-10-787-442-1
3 Sequence 1, Application US/10787442
4 Publication No. US20040260065A1
5 GENERAL INFORMATION:
6 APPLICANT: Novak, Julia E.
7 APPLICANT: Presnell, Scott R.
8 APPLICANT: Sprecher, Cindy A.
9 APPLICANT: Foester, Donald C.
10 APPLICANT: Holly, Richard D.
11 APPLICANT: Gross, Jane A.
12 APPLICANT: Johnston, Janet V.
13 APPLICANT: Nelson, Andrew J.
14 APPLICANT: Dillon, Stacey R.
15 APPLICANT: Hammond, Angela K.
16 TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND
17 FILE REFERENCE: 99-16
18 CURRENT APPLICATION NUMBER: US/10/787,442
19 CURRENT FILING DATE: 2004-02-26
20 PRIOR APPLICATION NUMBER: US/09/522,217
21 PRIOR FILING DATE: 2000-03-09
22 PRIOR APPLICATION NUMBER: US 60/123,547
23 PRIOR FILING DATE: 1999-03-09
24 PRIOR APPLICATION NUMBER: US 60/123,904

```

```

? PRIOR FILING DATE: 1999-03-11
? PRIOR APPLICATION NUMBER: US 60/142,013
? PRIOR FILING DATE: 1999-07-01
? NUMBER OF SEQ ID NOS: 115
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 1
? LENGTH: 642
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (47)...(532)
US-10-787-442-1

```

Query Match	74.0%;	Score 299.6;	DB 9;	Length 642;
Best Local Similarity	84.1%;	Pred. No. 1.7e-87;		
Matches 338;	Conservative 0;	Mismatches 64;	Indels 0;	Gaps 0;

QY	4	CAAGGTCAGAGATCGCACAATGTTGAAATGGGTCAACTTAATAGATAATGTTGATCAGCTG	63
Db	134	CAGGTCAGAGATCGCACAATGTTGAAATGGGTCAACTTAATAGATAATGTTGATCAGCTG	139
QY	64	AAAAATATATGTGAATGACCTGGTTCGGAAATTCCTCCGGCTCCGGAAGATGTTGAGACC	123
Db	194	AAAAATATATGTGAATGACCTGGTTCCTGAAATTCCTGCAAGTCCGGAAGATGTTGAGACA	253
QY	124	AACTGTGATGTGTCCTGGCTTTCTCTCGTGTTCAGAAAGCCGACGTGAATCCGGAAGACC	183
Db	254	AACGTGATGTGTCAGCTTTTTCGTGTTTCAAGAGGCCCAACTGAATGTCAGCAAAATACA	313
QY	184	GGTACAGAGAAAGTATCATCAACGTTTCCATTAATAAACTGAAGCTTAAACCGCGCTCC	243
Db	314	GGAAACAAATGAAGATTAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	373
QY	244	ACCAAGCAGAGTGTGTGTGAGAAACACCGTGTGACCTGCGCGTCTGTATTTATGAG	303
Db	374	ACAAATGACGGAGGAAGACAGAAACACAGACTTAACATCCCTCATGTGATTTCTTATGAG	433
QY	304	AAAAAAACCGCCGAAAAAGATTCCTGGAACGTTTCAAATCCCTGTGTGAGAAAAATGATTCAC	363
Db	434	AAAAAAACCAACCAAGAAATTCCTGAAGAAATTCCTGAATATCACTTCTCCAAAAGATATTCAT	493
QY	364	CAGCAGTGTCTCTGTATCCACGAGTTCCGGAAGATTCCTGA	405
Db	494	CAGCAGTGTCTCTGTATCCACGAGAAATGAAAGATTCCTGA	535

```

RESULT 12
US-10-951-239-1
: Sequence 1, Application US/10951239
: Publication No. US20050095223A1
: GENERAL INFORMATION:
: APPLICANT: Sivakumar, Pallavar
: APPLICANT: Nelson, Andrew
: TITLE OF INVENTION: METHODS OF TREATING AUTOIMMUNE DISEASES
: TITLE OF INVENTION: USING IL-21
: FILE REFERENCE: 03-09
: CURRENT APPLICATION NUMBER: US/10/951,239
: CURRENT FILING DATE: 2004-09-27
: PRIOR APPLICATION NUMBER: 60/505,919
: PRIOR FILING DATE: 2003-09-25
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 642
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: : LOCATION: (47)...(532)
US-10-951-239-1

```

Best Local Similarity 84.1%; Pred. No. 1.7e-87;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

```
OY 4 CAAGGTCAAGATGCCACATGATTAGATGCGTCAACTTATATGATTGTTGATCAGCTG 63
DB 134 CAAGGTCAAGATGCCACATGATTAGATGCGTCAACTTATATGATTGTTGATCAGCTG 193
OY 64 AAAATTTATGTAATGACTGTTCCGGAATTCCTGCGGCTCCGGAAGATTGTTAGACC 123
DB 194 AAAATTTATGTAATGACTGTTCCGGAATTCCTGCGGCTCCGGAAGATTGTTAGACA 253
OY 124 AACTGTGATGGTCCGCTTTCTCTGTTTCCAGAAAGCCAGCTGAAATCCGCAACACC 183
DB 254 AACTGTGATGGTCCGCTTTCTCTGTTTCCAGAAAGCCAGCTGAAATCCGCAACATACA 313
OY 184 GGTAAACAAGACGTATCATCAACGTTTCCATTAATAAACTGAAACGTAAACCGCGTCC 243
DB 314 GGAACCAATGAAAGGATATCAATGATATCAATTAAGCTGAAGGAAACCACTTCC 373
OY 244 ACCAAGCAGGTCTGTCGTCAAGAAACCGCTGACCTGCGCTCTGATTTCTATGAG 303
DB 374 ACAATGACGGAGAGAGACAGAAACAAGACTACATGCTTCAATGATTTCTATGAG 433
OY 304 AAAAACCAGCGAAGAAATTCCTGGAACGTTTCAATCCCTGCTGAGAAATGATTCAC 363
DB 434 AAAAACAACCCAAAGAAATTCCTAGAAAGATTCAATCACTTCTCAAAAAGATGATCAT 493
OY 364 CAGCAGCTGCTCTCTGTAACCCAGCTTCCGAAGATTCCTGA 405
DB 494 CAGCATCTGCTCTCTGTAACCAACAGGAAGTGAAGATTCCTGA 535
```

RESULT 13
US-11-174-398-1
Sequence 1, Application US/11174398
Publication No. US20050244930A1

GENERAL INFORMATION:
APPLICANT: Frennell, Scott R.
APPLICANT: West, James W.
APPLICANT: Novak, Julia E.
TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
FILE REFERENCE: 01-37
CURRENT APPLICATION NUMBER: US/11/174,398
CURRENT FILING DATE: 2005-07-01
PRIOR APPLICATION NUMBER: US/10/282,622
PRIOR FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 60/337,586
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 642
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (47) ... (532)
US-11-174-398-1

Query Match 74.0%; Score 299.6; DB 13; Length 642;
Best Local Similarity 84.1%; Pred. No. 1.7e-87;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

```
OY 4 CAAGGTCAAGATGCCACATGATTAGATGCGTCAACTTATATGATTGTTGATCAGCTG 63
DB 134 CAAGGTCAAGATGCCACATGATTAGATGCGTCAACTTATATGATTGTTGATCAGCTG 193
OY 64 AAAATTTATGTAATGACTGTTCCGGAATTCCTGCGGCTCCGGAAGATTGTTAGACC 123
DB 194 AAAATTTATGTAATGACTGTTCCGGAATTCCTGCGGCTCCGGAAGATTGTTAGACA 253
OY 124 AACTGTGATGGTCCGCTTTCTCTGTTTCCAGAAAGCCAGCTGAAATCCGCAACACC 183
DB 254 AACTGTGATGGTCCGCTTTCTCTGTTTCCAGAAAGCCAGCTGAAATCCGCAACACC 183
```

```
DB 254 AACTGTGATGGTCCAGCTTTTCTGTTTTCAGAAAGCCCACTAATAGTCAGCAATACA 313
OY 184 GGTAAACAAGACGTATCATCAACGTTTCCATTAATAAACTGAAACGTAAACCGCGTCC 243
DB 314 GGAACCAATGAAAGGATATCAATGATATCAATTAAGCTGAAGGAAACCACTTCC 373
OY 244 ACCAAGCAGGTCTGTCGTCAAGAAACCGCTGACCTGCGCTCTGATTTCTATGAG 303
DB 374 ACAATGACGGAGAGAGACAGAAACAAGACTACATGCTTCTCATGTTATTTATGAG 433
OY 304 AAAAACCAGCGAAGAAATTCCTGGAACGTTTCAATCCCTGCTGAGAAATGATTCAC 363
DB 434 AAAAACAACCCAAAGAAATTCCTAGAAAGATTCAATCACTTCTCAAAAAGTATTCAT 493
OY 364 CAGCAGCTGCTCTCTGTAACCCAGCTTCCGAAGATTCCTGA 405
DB 494 CAGCATCTGCTCTCTGTAACCAACAGGAAGTGAAGATTCCTGA 535
```

RESULT 14
US-11-134-489-1
Sequence 1, Application US/11134489
Publication No. US2005026596A1

GENERAL INFORMATION:
APPLICANT: Kindsvogel, Wayne R.
APPLICANT: Hughes, Steven D.
APPLICANT: Holly, Richard D.
APPLICANT: Clegg, Christopher H.
APPLICANT: Foster, Donald C.
APPLICANT: Johnson, Rebecca A.
APPLICANT: Heipel, Mark D.
TITLE OF INVENTION: METHODS OF TREATING CANCER USING IL-21 AND MONOCLONAL ANTIBODY
FILE REFERENCE: 04-03
CURRENT APPLICATION NUMBER: US/11/134,489
CURRENT FILING DATE: 2005-05-20
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 642
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (47) ... (532)
US-11-134-489-1

Query Match 74.0%; Score 299.6; DB 15; Length 642;
Best Local Similarity 84.1%; Pred. No. 1.7e-87;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

```
OY 4 CAAGGTCAAGATGCCACATGATTAGATGCGTCAACTTATATGATTGTTGATCAGCTG 63
DB 134 CAAGGTCAAGATGCCACATGATTAGATGCGTCAACTTATATGATTGTTGATCAGCTG 193
OY 64 AAAATTTATGTAATGACTGTTCCGGAATTCCTGCGGCTCCGGAAGATTGTTAGACC 123
DB 194 AAAATTTATGTAATGACTGTTCCGGAATTCCTGCGGCTCCGGAAGATTGTTAGACA 253
OY 124 AACTGTGATGGTCCGCTTTCTCTGTTTCCAGAAAGCCAGCTGAAATCCGCAACACC 183
DB 254 AACTGTGATGGTCCGCTTTCTCTGTTTCCAGAAAGCCAGCTGAAATCCGCAACATACA 313
OY 184 GGTAAACAAGACGTATCATCAACGTTTCCATTAATAAACTGAAACGTAAACCGCGTCC 243
DB 314 GGAACCAATGAAAGGATATCAATGATATCAATTAAGCTGAAGGAAACCACTTCC 373
OY 244 ACCAAGCAGGTCTGTCGTCAAGAAACCGCTGACCTGCGCTCTGATTTCTATGAG 303
DB 374 ACAATGACGGAGAGAGACAGAAACAAGACTACATGCTTCTCATGTTATTTATGAG 433
OY 304 AAAAACCAGCGAAGAAATTCCTGGAACGTTTCAATCCCTGCTGAGAAATGATTCAC 363
DB 434 AAAAACAACCCAAAGAAATTCCTAGAAAGATTCAATCACTTCTCAAAAAGTATTCAT 493
```

```
Db      434 AAAAAACCAACCAAGATTCTAGAAAAGATTCATCAATCACTTCCAAAAGATGATTCAT 493
QY      364 CAGCACTGTCTCTCTGCTACCCAGGTTCCGAAGATTCCTGA 405
Db      494 CAGCATCTGTCTCTTAGAACACAGGAAGTGAAGATTCCTGA 535
```

RESULT 15

```
US-11-137-807-11
; Sequence 11, Application US/11137807
; Publication No. US20060034810A1
; GENERAL INFORMATION:
; APPLICANT: Riley, James
; APPLICANT: June, Carl
; APPLICANT: vonderheide, Robert
; APPLICANT: Aquil, Nicole
; APPLICANT: Suhoski, Megan
; TITLE OF INVENTION: NOVEL ARTIFICIAL ANTIGEN PRESENTING CELLS AND USES THEREFOR
; FILE REFERENCE: 053893-5054US1
; CURRENT APPLICATION NUMBER: US/11/137,807
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/575,712
; PRIOR FILING DATE: 2004-05-27
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 611
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-137-807-11
```

```
Query Match      73.6%; Score 298; DB 16; Length 611;
Best Local Similarity 83.8%; Pred. No. 5.7e-87;
Matches 337; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY      4 CAAGTCAGATCGCCACATGATTAGATGCGTCACTTAATGATTTGATCAGCTG 63
Db      128 CAAGTCAGATCGCCACATGATTAGATGCGTCACTTAATGATTTGATCAGCTG 187
QY      64 AAAAATTATGTGAATGACTGTGTCGGAATTCTGCCGGCTCCGAAAGATTTGAGACC 123
Db      188 AAAAATTATGTGAATGACTGTGTCGGAATTCTGCCAGCTCCGAAAGATTTGAGACA 247
QY      124 AACTGTAGTGTGCGCTTCTCTGTTTCCAGAAAGCCAGCTGAATCCGCAACACC 183
Db      248 AACTGTAGTGTGCGCTTCTCTGTTTCCAGAAAGCCAGCTGAATCCGCAACATACA 307
QY      184 GGTAAACAAGACGTATCATCAAGTTTCAATTAAAAACTGAACGTAAACCGCGTCC 243
Db      308 GGAACCAATGAAGATTAATGATCAATTAAAAAGCTGAAGAGAAACCACTTCC 367
QY      244 ACCAAGCGAGTGTCTGTAGAAAACACGCTGACTGCGCGTCTGTGATTTATGAG 303
Db      368 ACAATGCAAGGAGAAAGACAGAAACACAGACTAACATGACCTTCATGTGATTTATGAG 427
QY      304 AAAAAACCGCGAAAGATTCCTGGAACGTTTCAATCCCTGCTGCAGAAAAATGATTCAC 363
Db      428 AAAAAACCGCGAAAGATTCCTGGAAGATTCATCAATCTTCGCAAAAGATGATTCAT 487
QY      364 CAGCACTGTCTCTCTGATCCAGGTTCCGAAGATTCCTGA 405
Db      488 CAGCATCTGTCTCTTAGAACACAGGAAGTGAAGATTCCTGA 529
```

Search completed: August 7, 2006, 12:30:07
Job time : 1012 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	405	100.0	405	6	US-10-735-49-27	Sequence 27, Appl
2	299.6	74.0	662	6	US-10-511-937-565	Sequence 565, Appl
3	299.6	74.0	662	6	US-10-735-149-1	Sequence 1, Appl
4	299.6	74.0	662	8	US-11-266-7488-401642	Sequence 401642, Appl
5	299.6	74.0	662	8	US-11-266-7488-472688	Sequence 472688, Appl
6	298	73.6	617	6	US-10-806-511-1	Sequence 1, Appl
7	182	44.9	3072	6	US-10-806-511-3	Sequence 3, Appl
8	64	15.6	64	6	US-10-735-149-26	Sequence 26, Appl
9	63	15.8	63	6	US-10-735-149-25	Sequence 25, Appl
10	60	14.8	60	6	US-10-735-149-17	Sequence 17, Appl
11	60	14.8	60	6	US-10-735-149-18	Sequence 18, Appl
12	60	14.8	60	6	US-10-735-149-19	Sequence 19, Appl
13	60	14.8	60	6	US-10-735-149-20	Sequence 20, Appl
14	60	14.8	60	6	US-10-735-149-21	Sequence 21, Appl
15	60	14.8	60	6	US-10-735-149-22	Sequence 22, Appl
16	58.4	14.4	60	6	US-10-735-149-16	Sequence 16, Appl
17	41	10.1	50	6	US-10-735-149-15	Sequence 15, Appl
18	40	9.9	40	6	US-10-735-149-11	Sequence 11, Appl
19	40	9.9	40	6	US-10-735-149-12	Sequence 12, Appl
20	36.8	9.1	40	6	US-10-735-149-9	Sequence 9, Appl
21	36.8	9.1	40	6	US-10-735-149-10	Sequence 10, Appl
22	36	8.9	60	6	US-10-735-149-23	Sequence 23, Appl
23	32.4	8.0	26087	9	US-11-021-937-19	Sequence 19, Appl

C	24	32.2	8.0	553	8	US-11-266-748A-271176	Sequence 271776,
	25	32.2	8.0	553	8	US-11-266-748A-332293	Sequence 332293,
C	26	32.2	8.0	724	8	US-11-266-748A-44600	Sequence 44600, A
	27	32.2	8.0	909	8	US-11-266-748A-85263	Sequence 85263, A
	28	32.2	8.0	909	8	US-11-266-748A-138074	Sequence 138074,
C	29	32.2	8.0	941	8	US-11-266-748A-219123	Sequence 219123,
	30	32.2	8.0	1594	8	US-11-266-748A-249298	Sequence 249298,
	31	32.2	8.0	2400	6	US-10-511-937-28287	Sequence 2837, Ap
	32	32.2	8.0	6455	8	US-11-266-748A-29566	Sequence 29566, A
C	33	32	7.9	446	8	US-11-266-748A-193446	Sequence 193446,
	34	32	7.9	446	8	US-11-266-748A-227054	Sequence 227054,
C	35	32	7.9	446	8	US-11-266-748A-241212	Sequence 241212,
	36	32	7.9	525	8	US-11-266-748A-58700	Sequence 58680, A
	37	32	7.9	1000	8	US-11-266-748A-385667	Sequence 385667,
	38	32	7.9	1000	8	US-11-266-748A-337116	Sequence 337116,
C	39	32	7.9	1000	8	US-11-266-748A-395967	Sequence 395967,
	40	32	7.9	1000	8	US-11-266-748A-467013	Sequence 467013,
C	41	32	7.9	1113	8	US-11-266-748A-227053	Sequence 227053,
	42	32	7.9	1587	8	US-11-266-748A-206672	Sequence 206672, A
C	43	32	7.9	1587	8	US-11-266-748A-62533	Sequence 62533, A
	44	32	7.9	1587	8	US-11-266-748A-65372	Sequence 65372, A
C	45	31.2	7.7	138627	6	US-10-540-899-1519	Sequence 159, App

ALIGNMENTS

RESULT 1
US-10-735-149-27

```

Sequence 27, Application US/10735149
Publication No. US20060134754A1
GENERAL INFORMATION:
APPLICANT: Chan, Chung
APPLICANT: Zamost, Bruce L.
APPLICANT: Coverit, Douglas C.
APPLICANT: Liu, Hong Y.
APPLICANT: De Jongh, Karen S.
APPLICANT: Meyer, Jeffrey D.
APPLICANT: Holdeman, Susan D.
TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21
TITLE OF INVENTION: IN A PROKARYOTIC HOST
FILE REFERENCE: 02-12
CURRENT APPLICATION NUMBER: US/10/735,149
CURRENT FILING DATE: 2003-12-12
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 27
LENGTH: 405
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: optimized IL-21
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(405)
US-10-735-149-27

```

Query Match	100.0%;	Score 405;	DB 6;	Length 405;
-------------	---------	------------	-------	-------------

```
Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy	1	ANGCAAGGTCAAGATTCGCCACATGATTTGAATGGGTCAACTTATAGATATTTGTGTGATCAG	60
Db	1	ANGCAAGGTCAAGATTCGCCACATGATTTGAATGGGTCAACTTATAGATATTTGTGTGATCAG	60
Qy	61	CTGAAAAAATTAATGTAATAGACTGTTCGCCGAATTCCTCGCCGCTCCGGAAAGATGTTGAG	120
Db	61	CTGAAAAAATTAATGTAATAGACTGTTCGCCGAATTCCTCGCCGCTCCGGAAAGATGTTGAG	120
Qy	121	ACCAACTGTAGTGTGTCGCTTTCTCTGTTTCCAGAAAGCCACGTGAATAATCCGCAAC	180
Db	121	ACCAACTGTAGTGTGTCGCTTTCTCTGTTTCCAGAAAGCCACGTGAATAATCCGCAAC	180

```
QY 181 ACCGGTAACACGACGATCATCAAGTTTCATTAAAAAACTGAAACGTAAACCGCGC 240
|
|
|
Db 181 ACCGGTAACACGACGATCATCAAGTTTCATTAAAAAACTGAAACGTAAACCGCGC 240
QY 241 TCACCAACGACGATGCTGCTGACAAACACCGCTGACCTGCGCTGCTGATTTAT 300
|
|
|
Db 241 TCACCAACGACGATGCTGCTGACAAACACCGCTGACCTGCGCTGCTGATTTAT 300
QY 301 GAGAAAAACCGCGAAGAAATTCCTGGAACGTTCAAAATCCGCTGACAGAAATGAT 360
|
|
|
Db 301 GAGAAAAACCGCGAAGAAATTCCTGGAACGTTCAAAATCCGCTGACAGAAATGAT 360
QY 361 CACGACACCTGCTCTCTCGTACCCACGCTTCGGAAGATTCCTGA 405
|
|
|
Db 361 CACGACACCTGCTCTCTCGTACCCACGCTTCGGAAGATTCCTGA 405

RESULT 2
US-10-511-937-565
; Sequence 565, Application US/10511937
; Publication No. US2006088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 565
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-565

Query Match 74.0%; Score 299.6; DB 6; Length 642;
Best Local Similarity 84.1%; Pred. No. 2.6e-91;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 4 CAAGTCAGATCGCACATGATTAGATGCGTCAACTTATAGATTGTTGATCACTG 63
|
|
|
Db 134 CAAGTCAGATCGCACATGATTAGATGCGTCAACTTATAGATTGTTGATCACTG 193
QY 64 AAAAAATTATGTAATGACCTGCTCCGGAATTCCTGCCGCTCGGAAGATGTTGAG 123
|
|
|
Db 194 AAAAAATTATGTAATGACCTGCTCCGGAATTCCTGCCGCTCGGAAGATGTTGAG 253
QY 124 AACTGTAGTGTGCTGCTGCTTCTCTGTTTCCAGAAAGCCGACGTGAAGTCCG 183
|
|
|
Db 254 AACTGTAGTGTGCTGCTGCTTCTCTGTTTCCAGAAAGCCGACGTGAAGTCCG 313
QY 184 GGTAAACGAAAGTATCATCAAGTTTCATTAAAAAAGTAAACGTAACCGCGCTCC 243
|
|
|
Db 314 GGAACCAATGAAAGATATCAATGATCAATTAAGTGAAGGAGAAACCACTTCC 373
QY 244 ACCAAGCAGGTGCTGCTGACAAACACCGTCTGACCTGCTGCTGATTTTATGAG 303
|
|
|
Db 374 ACAATGCAAGGAGAAAGACGAAACACGACTAACTAATGCTCCTTATGATTTATGAG 433
```

```
QY 304 AAAAAACCGCGAAGAAATTCCTGGAACGTTCAAAATCCCTGCTGACAGAAATGATTCAC 363
|
|
|
Db 434 AAAAAACCGCGAAGAAATTCCTGGAAGATTCATTAATCACTTCCAAAAGATGATTCAT 493
QY 364 CAGACCTGCTCTCTGTAACCGGTTCCGAAGATTCCTGA 405
|
|
|
Db 494 CAGACCTGCTCTCTGTAACCAACGGAAGTGAAGATTCCTGA 535

RESULT 3
US-10-735-149-1
; Sequence 1, Application US/10735149
; Publication No. US2006013475A1
; GENERAL INFORMATION:
; APPLICANT: Chan, Chung
; APPLICANT: Zamost, Bruce L.
; APPLICANT: Covert, Douglas C.
; APPLICANT: Liu, Hong Y.
; APPLICANT: De Jongh, Karen S.
; APPLICANT: Meyer, Jeffrey D.
; APPLICANT: Holderman, Susan D.
; TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21
; TITLE OF INVENTION: IN A PROKARYOTIC HOST
; FILE REFERENCE: 02-12
; CURRENT APPLICATION NUMBER: US/10/735,149
; CURRENT FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (47)...(535)
US-10-735-149-1

Query Match 74.0%; Score 299.6; DB 6; Length 642;
Best Local Similarity 84.1%; Pred. No. 2.6e-91;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 4 CAAGTCAGATCGCACATGATTAGATGCGTCAACTTATAGATTGTTGATCACTG 63
|
|
|
Db 134 CAAGTCAGATCGCACATGATTAGATGCGTCAACTTATAGATTGTTGATCACTG 193
QY 64 AAAAAATTATGTAATGACCTGCTCCGGAATTCCTGCCGCTCGGAAGATGTTGAG 123
|
|
|
Db 194 AAAAAATTATGTAATGACCTGCTCCGGAATTCCTGCCGCTCGGAAGATGTTGAG 253
QY 124 AACTGTAGTGTGCTGCTGCTTCTCTGTTTCCAGAAAGCCGACGTGAAGTCCG 183
|
|
|
Db 254 AACTGTAGTGTGCTGCTGCTTCTCTGTTTCCAGAAAGCCGACGTGAAGTCCG 313
QY 184 GGTAAACGAAAGTATCATCAAGTTTCATTAAAAAAGTAAACGTAACCGCGCTCC 243
|
|
|
Db 314 GGAACCAATGAAAGATATCAATGATCAATTAAGTGAAGGAGAAACCACTTCC 373
QY 244 ACCAAGCAGGTGCTGCTGACAAACACCGTCTGACCTGCTGCTGATTTTATGAG 303
|
|
|
Db 374 ACAATGCAAGGAGAAAGACGAAACACGACTAATGCTCCTTATGATTTATGAG 433
QY 304 AAAAAACCGCGAAGAAATTCCTGGAACGTTCAAAATCCCTGCTGACAGAAATGATTCAC 363
|
|
|
Db 434 AAAAAACCGCGAAGAAATTCCTGGAAGATTCATTAATCACTTCCAAAAGATGATTCAT 493
QY 364 CAGACCTGCTCTCTGTAACCGGTTCCGAAGATTCCTGA 405
|
|
|
Db 494 CAGACCTGCTCTCTGTAACCAACGGAAGTGAAGATTCCTGA 535

RESULT 4
US-11-266-748A-401642
; Sequence 401642, Application US/11266748A
```

```
; Publication No. US2006013463A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 401642
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-11-266-748A-401642

Query Match      74.0%; Score 299.6; DB 8; Length 642;
Best Local Similarity 84.1%; Pred. No. 2.6e-91;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 4 CAAGTCAAGATCGGCACATGATTAAGATGCGTCACTTAATGATTTGATGATCAGCTG 63
DB 134 CAAGTCAAGATCGGCACATGATTAAGATGCGTCACTTAATGATTTGATGATCAGCTG 193
QY 64 AAAAATTTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 123
DB 194 AAAAATTTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 253
QY 124 AACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 183
DB 254 AACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 313
QY 184 GGTAAACAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 243
DB 314 GGAATCAATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 373
QY 244 ACCAAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 303
DB 374 ACAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 433
QY 304 AAAAACCAGCGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 363
DB 434 AAAAACCAGCGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 493
QY 364 CAGCAGCTGTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 405
DB 494 CAGCAGCTGTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 535

RESULT 5
US-11-266-748A-472688/c
; Sequence 472688, Application US/11266748A
; Publication No. US2006013463A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
```

```
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 472688
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-11-266-748A-472688

Query Match      74.0%; Score 299.6; DB 8; Length 642;
Best Local Similarity 84.1%; Pred. No. 2.6e-91;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 4 CAAGTCAAGATCGGCACATGATTAAGATGCGTCACTTAATGATTTGATGATCAGCTG 63
DB 509 CAAGTCAAGATCGGCACATGATTAAGATGCGTCACTTAATGATTTGATGATCAGCTG 450
QY 64 AAAAATTTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 123
DB 449 AAAAATTTGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 390
QY 124 AACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 183
DB 389 AACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 330
QY 184 GGTAAACAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 243
DB 329 GGAATCAATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 270
QY 244 ACCAAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 303
DB 269 ACAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 210
QY 304 AAAAACCAGCGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 363
DB 209 AAAAACCAGCGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 150
QY 364 CAGCAGCTGTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 405
DB 149 CAGCAGCTGTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 108

RESULT 6
US-10-806-611-1
; Sequence 1, Application US/10806611
; Publication No. US20060159655A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Chin, Elaine Y.
; APPLICANT: Senicee, Mayra
; APPLICANT: Young, Deborah A.
```



```

? TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF
? TITLE OF INVENTION: INTERLEUKIN-21/ INTERLEUKIN-21 RECEPTOR
? FILE REFERENCE: 16158-013001
? CURRENT APPLICATION NUMBER: US/10/806,611
? CURRENT FILING DATE: 2004-03-22
? PRIOR APPLICATION NUMBER: US 60/456,920
? PRIOR FILING DATE: 2003-03-21
? NUMBER OF SEQ ID NOS: 13
? SOFTWARE: Patentin version 3.2
? SEQ ID NO 1
? LENGTH: 617
? TYPE: DNA
? ORGANISM: Homo sapiens
? US-10-806-611-1

```

Query Match	73.6%	Score 298	DB 61	length 617
Best Local Similarity	83.8%	Pred. No. 8.9e-91		
Matches 337	Conservative	0	Mismatches 65	Indels 0
				Gaps 0

QY	4	CAAGGCTCAAGATGCGCACATGATTGGAATGCGTCAACTTATAGATATGTTGATCACTG	63
Db	134	CAAGGCTCAAGATGCGCACATGATTGGAATGCGTCAACTTATAGATATGTTGATCACTG	133
QY	64	AAAAATTAATGTGAATGACCTGGTCCGGAATTCCTGCGCGCTCCGGAAGATGTTGAGACC	123
Db	194	AAAAATTAATGTGAATGACCTGGTCCGGAATTCCTGCGCGCTCCGGAAGATGTTGAGACA	253
QY	124	AATGTGATGATGGTCCGCTTTCTCTGTTTCCAGAAAGCCAGCTGGAATCCGCAACAAC	183
Db	254	AATGTGATGATGGTCCGCTTTCTCTGTTTCCAGAAAGCCAGCTGGAATCCGCAAAAACA	313
QY	184	GGTAAACAAGAAAGTATCATCAACGTTTCATTAAAAACGTAAACGTAAACGCGCGTCC	243
Db	314	GGAAACAATGAAGAATTAATCAATGATATCAATTAATAAAAGCTGAAGAGAAACCACTTCC	373
QY	244	ACCAACGACAGTGTGTCGTGAGAAACAACGCTCTGACCTCCGTCCTGTGATTCCTATGAG	303
Db	374	ACCAATGACAGGAGGAAGACAGAAACAACGACTTAACATCCCTTCATGTGATTCCTATGAG	433
QY	304	AAAAAAACCGCCGAAGAATTCCTGGAAGCTTCAATCCCTGCTGCGAAGAAATGATTCAC	363
Db	434	AAAAAAACCAACCAAAATAATTCCTAGAAAGATTCAAATCACTTCCTCAAAAGATGATTCAT	493
QY	364	CAGACCTGTCTCTCTGTACCAACGCTTCCGAAGATTCCTGA	405
Db	494	CAGCATCTGTCTCTTAGAACAACAGGAAGTGAAGATTCCTGA	535

```

RESULT 7
US-10-806-611-3
; Sequence 3, Application US/10806611
; Publication No. US20060159655A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Chin, Elaine Y.
; APPLICANT: Senices, Mayra
; APPLICANT: Young, Deborah A.
; TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF
; TITLE OF INVENTION: INTERLEUKIN-21/ INTERLEUKIN-21 RECEPTOR
; FILE REFERENCE: 16158-013001
; CURRENT APPLICATION NUMBER: US/10/806,611
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: US 60/456,920
; PRIOR FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 3072
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-806-611-3

```

Best Local Similarity 67.4%; Pred. No. 5e-51;
Matches 271; Conservative 0; Mismatches 130; Indels 1; Gaps 1.

QY 4 AAGGTCAAGATCCGCACATGATTGAATGCGTCAACTAATGATATTTGATCAGCTG 63
 Db 120 CAAAGGCCAGATCCGCTCTCTGATTGACTTGGCTACCTTATTGACATTGTTGAACAGCTG 179
 QY 64 AAAAAATTATGTGAATGACCTGGTTCCGGAATTCCTCGCCGCTCCGGGAAGATGTTGAGACC 123
 Db 180 AAAATCTATGAAAAATGACCTGGATCTTGAACTTATCATGAGCTCCACCAAGATGTAAGGGG 239
 QY 124 AACTGTGATGTCGCGCTTTTCTCCCTGTTTCCAGAAAGCCAGCTGAATCCGCAACACC 183
 Db 240 CACTGTGAGCATGACAGCTTTTGGCCGTGTTTCAGAAAGCCAACTCAAGCATCAACCCCT 299
 QY 184 GGTAAACAAGAACGATCATCATCAAGTTTCCATTAAAACTGAAACGTAAACCGCCGCTCC 243
 Db 300 GGAACCATTAAGACATTATCATCTTAACCTCTGGGCCAGCTACGAGAGAGGCTGCTGGCC 359
 QY 244 ACCAAGCAGAGTCTGTCGTACAGAAACCCGCTGACCTGCCCCTGTGATTTCTTATGAG 303
 Db 360 AGGAGGGGAGAAAAAGAAACAGAGACATAGCTAATATGCCCTTCCTGTAATTCGTATGAG 419
 QY 304 AAAAAACCGCCGAAGAATTCTGTGAACGTTTCAATCTCTGCTGACGAAATGATTCAC 363
 Db 420 AAAAGGACACCCCAAGAAATTCCTTAAGAAAGACTTAAATGCTCTTCCAAAAGATGATTCAT 479
 QY 364 CAGACCTGTCTCTCTGTACCAAGGTTCCGAAGATTCCTGA 405
 Db 480 CAGCATCTCTCTTGAACACATTA-GGACCCGAAGATTCCTGA 520

RESULT 8
US-10-735-149-26

```

Publication No. US20060134754A1
GENERAL INFORMATION:
APPLICANT: Chan, Chung
APPLICANT: Zamost, Bruce L.
APPLICANT: Covert, Douglas C.
APPLICANT: Liu, Hong Y.
APPLICANT: De Jongh, Karen S.
APPLICANT: Meyer, Jeffrey D.
APPLICANT: Holdeman, Susan D.
TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21
TITLE OF INVENTION: IN A PROKARYOTIC HOST
FILE REFERENCE: 02-12
CURRENT APPLICATION NUMBER: US/10/735,149
CURRENT FILING DATE: 2003-12-12
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26
LENGTH: 64
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: oligonucleotide ZC40107
US-10-735-149-26

```

Query Match	15.8%;	Score 64;	DB 6;	Length 64;
Best Local Similarity	100.0%;	Pred. No. 7.2e-12;		
Matches 64;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Oy	TTATAGATATTGTGATCAGCTGAATAAATTATGTAAATGACTGGTTCGGAAATTCCTGC	100
Dd	1 TTAATGATATTGTGATCAGCTGAATAAATTATGTAAATGACTGGTTCGGAAATTCCTGC	60
Oy	CGGC	104
Dd	CGGC	64

Query Match 44.9%; Score 182; DB 6; Length 3072;


```
US-10-735-149-25/c
; Sequence 25, Application US/10735149
; Publication No. US20060134754A1
; GENERAL INFORMATION:
; APPLICANT: Chan, Chung
; APPLICANT: Zamost, Bruce L.
; APPLICANT: Covert, Douglas C.
; APPLICANT: Liu, Hong Y.
; APPLICANT: De Jongh, Karen S.
; APPLICANT: Meyer, Jeffrey D.
; APPLICANT: Holderman, Susan D.
; TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21
; FILE REFERENCE: 02-12
; CURRENT APPLICATION NUMBER: US/10/735,149
; CURRENT FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 63
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide ZC40133
US-10-735-149-25

Query Match      15.6%; Score 63; DB 6; Length 63;
Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      58 CAGCTGAAATTTGTAAGTGAAGTCTGTCGGAATTCGCGGCTCCGGAAGATTT 117
Db      63 CAGCTGAAATTTGTAAGTGAAGTCTGTCGGAATTCGCGGCTCCGGAAGATTT 4

Cy      118 GAG 120
Db      3 GAG 1

RESULT 10
US-10-735-149-17/c
; Sequence 17, Application US/10735149
; Publication No. US20060134754A1
; GENERAL INFORMATION:
; APPLICANT: Chan, Chung
; APPLICANT: Zamost, Bruce L.
; APPLICANT: Covert, Douglas C.
; APPLICANT: Liu, Hong Y.
; APPLICANT: De Jongh, Karen S.
; APPLICANT: Meyer, Jeffrey D.
; APPLICANT: Holderman, Susan D.
; TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21
; FILE REFERENCE: 02-12
; CURRENT APPLICATION NUMBER: US/10/735,149
; CURRENT FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide ZC22965
US-10-735-149-17

Query Match      14.8%; Score 60; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      110 AAGATGTTGAGACCAACTGTGAGTGTCCGCTTTCTCGTTTCAGAAAGCCGAGCTGA 169
Db      60 AAGATGTTGAGACCAACTGTGAGTGTCCGCTTTCTCGTTTCAGAAAGCCGAGCTGA 1
```

```
RESULT 11
US-10-735-149-18
; Sequence 18, Application US/10735149
; Publication No. US20060134754A1
; GENERAL INFORMATION:
; APPLICANT: Chan, Chung
; APPLICANT: Zamost, Bruce L.
; APPLICANT: Covert, Douglas C.
; APPLICANT: Liu, Hong Y.
; APPLICANT: De Jongh, Karen S.
; APPLICANT: Meyer, Jeffrey D.
; APPLICANT: Holderman, Susan D.
; TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21
; FILE REFERENCE: 02-12
; CURRENT APPLICATION NUMBER: US/10/735,149
; CURRENT FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide ZC22966
US-10-735-149-18

Query Match      14.8%; Score 60; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      150 TTTCAGAAAGCCAGCTGAATTCGCAACACCGGTAAACGAGCAATCATCACT 209
Db      1 TTTCAGAAAGCCAGCTGAATTCGCAACACCGGTAAACGAGCAATCATCACT 60

RESULT 12
US-10-735-149-19/c
; Sequence 19, Application US/10735149
; Publication No. US20060134754A1
; GENERAL INFORMATION:
; APPLICANT: Chan, Chung
; APPLICANT: Zamost, Bruce L.
; APPLICANT: Covert, Douglas C.
; APPLICANT: Liu, Hong Y.
; APPLICANT: De Jongh, Karen S.
; APPLICANT: Meyer, Jeffrey D.
; APPLICANT: Holderman, Susan D.
; TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21
; FILE REFERENCE: 02-12
; CURRENT APPLICATION NUMBER: US/10/735,149
; CURRENT FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide ZC22967
US-10-735-149-19

Query Match      14.8%; Score 60; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      190 AACGAGTATCATCAACGTTCCATTAAATACTGAACGTAACCGCGCTCCACCAAC 249
Db      60 AACGAGTATCATCAACGTTCCATTAAATACTGAACGTAACCGCGCTCCACCAAC 1
```

RESULT 13

US-10-735-149-20
; Sequence 20, Application US/10735149
; Publication No. US20060134754A1
; GENERAL INFORMATION:
; APPLICANT: Chan, Chung
; APPLICANT: Zamost, Bruce L.
; APPLICANT: Covert, Douglas C.
; APPLICANT: Liu, Hong Y.
; APPLICANT: De Jongh, Karen S.
; APPLICANT: Meyer, Jeffrey D.
; APPLICANT: Holderman, Susan D.
; TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21
; FILE REFERENCE: 02-12
; CURRENT APPLICATION NUMBER: US/10/735,149
; CURRENT FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide ZC22968
US-10-735-149-20

Query Match 14.8%; Score 60; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 250 GCAGGTGCTGTGCAAAACCCGTCGACCCCGCCGTCGTGTTCTTATGAGAAAAA 309
Db 1 GCAGGTGCTGTGCAAAACCCGTCGACCTGCGTCGTGTTCTTATGAGAAAAA 60

RESULT 14

US-10-735-149-21/C
; Sequence 21, Application US/10735149
; Publication No. US20060134754A1
; GENERAL INFORMATION:
; APPLICANT: Chan, Chung
; APPLICANT: Zamost, Bruce L.
; APPLICANT: Covert, Douglas C.
; APPLICANT: Liu, Hong Y.
; APPLICANT: De Jongh, Karen S.
; APPLICANT: Meyer, Jeffrey D.
; APPLICANT: Holderman, Susan D.
; TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21
; FILE REFERENCE: 02-12
; CURRENT APPLICATION NUMBER: US/10/735,149
; CURRENT FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide ZC22969
US-10-735-149-21

Query Match 14.8%; Score 60; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 290 GTGATTTCTTATGAGAAAAACCGCGAAAGATTCCGTGAAACGTTCAAAATCCCTGCTGC 349
Db 60 GTGATTTCTTATGAGAAAAACCGCGAAAGATTCCGTGAAACGTTCAAAATCCCTGCTGC 1

RESULT 15

US-10-735-149-22
; Sequence 22, Application US/10735149
; Publication No. US20060134754A1
; GENERAL INFORMATION:
; APPLICANT: Chan, Chung
; APPLICANT: Zamost, Bruce L.
; APPLICANT: Covert, Douglas C.
; APPLICANT: Liu, Hong Y.
; APPLICANT: De Jongh, Karen S.
; APPLICANT: Meyer, Jeffrey D.
; APPLICANT: Holderman, Susan D.
; TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21
; FILE REFERENCE: 02-12
; CURRENT APPLICATION NUMBER: US/10/735,149
; CURRENT FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide ZC22970
US-10-735-149-22

Query Match 14.8%; Score 60; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 330 ACCTTTCAATTCCTGCTGCAAAATGATTACACGACCTGTCCTCTGTAACCCACGG 389
Db 1 ACCTTTCAATTCCTGCTGCAAAATGATTACACGACCTGTCCTCTGTAACCCACGG 60

Search completed: August 7, 2006, 14:03:08
Job time : 1538 secs

QY 244 ACCAAGCAGATGTCGTGCAAGAAACACGGTCGACCTGCGCTGNGATTCTTATGAG 303
Db 322 ACAATGACAGGAGAAACAGAAACACAGACTAATGAGCCCTTATGATGATTTATGAG 381
QY 304 AAAAAACCGCGAAGAAATTCCTGGAACGTTTCAAAATCCCTGCTGCAGAAATGATTCAC 363
Db 382 AAAAAACCAACCAAGAAATTCCTGGAAGAAATTCCTGCAATTCCTCAAAAAGATGATTCAT 441
QY 364 CAGCACTGTCTCTGCTGACCAACGCTTCGGAAGATTCCTGA 405
Db 442 CAGCATCTGTCTCTGACACACAGAAAGTGAAGATTCCTGA 483

RESULT 2
BD248998 483 bp DNA linear PAT 17-JUL-2003
LOCUS Novel cytokine ZALPHA11 ligand.
ACCESSION BD248998 GI:33058768
VERSION JP 2002537839-A/59.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 483)
AUTHORS Novak,J.E., Prensell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D., Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and Hammond,A.K.
TITLE Novel cytokine ZALPHA11 ligand
JOURNAL Patent: JP 2002537839-A 59 12-NOV-2002;
COMMENT ZYMOGENETICS INC
OS Homo sapiens (human)
EN JP 2002537839-A/59
PD 12-NOV-2002
PF 09-MAR-2000 JP 2000603382
PR 09-MAR-1999 US 09/264908, 11-MAR-1999 US 09/265992 PR
PI JUL-1999 US 60/142013 PRESNELL, CINDY A SPRECHER, DONALD C PI
FOSTER,
PI RICHARD D HOLLY,JANE A GROSS,JANET V JOHNSTON,ANDREW J NELSON,
PI STACEY R DILLON,ANGELA K HAMMOND
PC C12N15/09,A61K38/00,A61K45/00,A61J35/00,A61J37/00,C07K14/52,
PC C07K14/53,
PC C07K14/54,C07K14/55,C07K16/24,C07K19/00,C12N1/15,C12N1/19, PC
C12N1/21,
PC C12N5/10,C12P21/02,C12P21/02,G01N33/53,C12N15/00,C12N5/00, PC
A61K37/02
CC Novel cytokine ZALPHA11 ligand
FH Key Location/Qualifiers
FT source 1..483
FT Location/Qualifiers
1..483
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 74.0%; Score 299.6; DB 2; Length 483;
Best Local Similarity 84.1%; Pred. No. 3.7e-92;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Db 202 AACTGTAGTGTGTCAGCTTTTCTGTTTCAGAAAGCCCACTAAAGTCAGCAAAATACA 261
QY 184 GGTACACAGAAAGTATCATCAAGCTTTCATTTAAAAACTGAAACCTAAACCGCGCTCC 243
Db 262 GGAACCATGAAAGAAATCAATGATCAATTTAAAGCTGAAAGAAACCAACCTTCC 321
QY 244 ACCAAGCAGATGTCGTGCAAGAAACACGGTCGACCTGCGCTGCTGATTTCTTATGAG 303
Db 322 ACAATGACAGGAGAAACAGAAACACAGACTAATGAGCCCTTATGATGATTTATGAG 381
QY 304 AAAAAACCGCGAAGAAATTCCTGGAACGTTTCAAAATCCCTGCTGCAGAAATGATTCAC 363
Db 382 AAAAAACCAACCAAGAAATTCCTGGAAGAAATTCCTGCAATTCCTCAAAAAGATGATTCAT 441
QY 364 CAGCACTGTCTCTGCTGACCAACGCTTCGGAAGATTCCTGA 405
Db 442 CAGCATCTGTCTCTGACACACAGAAAGTGAAGATTCCTGA 483

RESULT 3
AR374097 483 bp DNA linear PAT 18-DEC-2003
LOCUS Sequence 63 from Patent US 6605272.
ACCESSION AR374097
VERSION AR374097.1 GI:40076669
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 483)
AUTHORS Novak,J.E., Prensell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D., Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and Hammond,A.K.
TITLE Methods of using zalphall 1 ligand
JOURNAL Patent: US 6605272-A 63 12-AUG-2003;
COMMENT ZymoGenetics, Inc.; Seattle, WA
FEATURES
source 1..483
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 74.0%; Score 299.6; DB 2; Length 483;
Best Local Similarity 84.1%; Pred. No. 3.7e-92;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Db 442 CAGCATCTGCTCCTTAGAACACGAGAGTAGATTCCTGA 483

RESULT 4
LOCUS AR456247 483 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 63 from patent US 6686178.
ACCESSION AR456247
VERSION AR456247.1 GI:42691270
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 483)
AUTHORS Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
Grobs,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
Hammond,A.K.
TITLE Cytokine zalphal1 ligand polynucleotides
JOURNML Patent: US 6686178-A 63 03-FEB-2004;
FEATURES
source Location/Qualifiers
1..483
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 74.0%; Score 299.6; DB 2; Length 483;
Best Local Similarity 84.1%; Pred. No. 3.7e-92;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 4 CAAGTCAGAGTCCGCACATGATTAGATGCTCAACTTATGATTTGATCAGCTG 63
Db 82 CAAGTCAGAGTCCGCACATGATTAGATGCTCAACTTATGATTTGATCAGCTG 141
Qy 64 AAAAATTATGTAATGATGACTGCTGCTCCGGAATTCCTGCGGCTCCGGAAGATGTTAGACC 123
Db 142 AAAAATTATGTAATGATGACTGCTCCCTGAATTTCTGCGAGCTCCGGAAGATGTTAGACA 201
Qy 124 AACTGTGAGTGGTCCGCTTTCTCTGTTTCCAGAAAGCCAGCTGAAATCCGCAAAACC 183
Db 202 AACTGTGAGTGGTCCGCTTTTCTGTTTCCAGAAAGCCAGCTGAAATGCA 261
Qy 184 GGTAAACAAGAACATGATCAATCACTTTCAATTAAGAAAGCTGAAAGCCGCTCC 243
Db 262 GGAACCAATGAAAGATATCAATGATTAATTAAGAAAGCTGAAAGCAACCTTCC 321
Qy 244 ACCAAGCAGAGTCCGCTCAGAAACACGCTGACCTGCGCTGATGATTTATGAG 303
Db 322 ACAATGCGGAGAGACAGAACACAGACTAACATGCCCTTCATGTGATTTCTATGAG 381
Qy 304 AAAAACCAGCGAAGAAATTCCTGGAACGTTTCAATCCCTGCTGAGAAATGATTCAC 363
Db 382 AAAAACCAGCGAAGAAATTCCTGGAAGATTCATCAATCACTTCTCAAAAGATGATTCAT 441
Qy 364 CAGCAGCTGCTCTCTGTAACCAAGCTTCCGAAGATTCCTGA 405
Db 442 CAGCATCTGCTCCTTAGAACACACGAGAGTAGATTCCTGA 483

RESULT 5
LOCUS DD180237 489 bp DNA linear PAT 19-DEC-2005
DEFINITION Albumin Fusion Proteins.
ACCESSION DD180237
VERSION DD180237.1 GI:83973219
KEYWORDS UP 2005514060-A/1222.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 489)
AUTHORS Haseltine,W.A., Rosen,C.A., Ballance,D.J. and Turner,A.J.

TITLE Albumin Fusion Proteins
JOURNML Patent: UP 2005514060-A/1222 19-MAY-2005;
COMMENT Human Genome Sciences Inc,Delta Biotechnology Limited, Principia
Pharmaceutical Corporation
OS Homo sapiens
PN UP 2005514060-A/1222
PD 19-MAY-2005
PF 23-DEC-2002 JP 2003560158
PR 24-JUL-2002 US 60/398008,09-AUG-2002 US 60/402131, PR
23-OCT-2002 US 60/420246,02-OCT-2002 US 60/414964, PR
18-SEP-2002 US 60/411355,18-SEP-2002 US 60/411426, PR
13-AUG-2002 US 60/402708,11-OCT-2002 US 60/417611, PR
05-NOV-2002 US 60/423623,10-JUL-2002 US 60/394625, PR
05-JUN-2002 US 60/385708,28-MAY-2002 US 60/383123, PR
21-DEC-2001 US 60/341811,28-JAN-2002 US 60/351360, PR
08-APR-2002 US 60/370227,27-MAR-2002 US 60/367500, PR
28-FEB-2002 US 60/360000,26-FEB-2002 US 60/359370, PR
24-JAN-2002 US 60/350358,10-MAY-2002 US 60/378950, PR
24-MAY-2002 US 60/382617
PI William a haseltine,craig a rosen,david james ballance,andrew
PI john turner
CC

FEATURES
source Location/Qualifiers
1..489
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 74.0%; Score 299.6; DB 2; Length 489;
Best Local Similarity 84.1%; Pred. No. 3.7e-92;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 4 CAAGTCAGAGTCCGCACATGATTAGATGCTCAACTTATGATTTGATCAGCTG 63
Db 88 CAAGTCAGAGTCCGCACATGATTAGATGCTCAACTTATGATTTGATCAGCTG 147
Qy 64 AAAAATTATGTAATGATGACTGCTCCGGAATTCCTGCGGCTCCGGAAGATGTTAGACC 123
Db 148 AAAAATTATGTAATGATGACTGCTCCCTGAATTTCTGCGAGCTCCGGAAGATGTTAGACA 207
Qy 124 AACTGTGAGTGGTCCGCTTTCTCTGTTTCCAGAAAGCCAGCTGAAATCCGCAAAACC 183
Db 208 AACTGTGAGTGGTCCGCTTTTCTGTTTCCAGAAAGCCAGCTGAAATGCA 267
Qy 184 GGTAAACAAGAACATGATCAATCACTTTCAATTAAGAAAGCTGAAAGCCGCTCC 243
Db 268 GGAACCAATGAAAGATATCAATGATTAATTAAGAAAGCTGAAAGCAACCTTCC 327
Qy 244 ACCAAGCAGAGTCCGCTCAGAAACACGCTGACCTGCGCTGATGATTTCTATGAG 303
Db 328 ACAATGCGGAGAGACAGAACACAGACTAACATGCCCTTCATGTGATTTCTATGAG 387
Qy 304 AAAAACCAGCGAAGAAATTCCTGGAACGTTTCAATCCCTGCTGAGAAATGATTCAC 363
Db 388 AAAAACCAGCGAAGAAATTCCTGGAAGATTCATCAATCACTTCTCAAAAGATGATTCAT 447
Qy 364 CAGCAGCTGCTCTCTGTAACCAAGCTTCCGAAGATTCCTGA 405
Db 448 CAGCATCTGCTCCTTAGAACACACGAGAGTAGATTCCTGA 489

RESULT 6
LOCUS BC066260 564 bp mRNA linear PRI 08-MAR-2005
DEFINITION Homo sapiens interleukin 21, mRNA (cDNA clone MGC:79378
IMAGE:6971863), complete cds.
ACCESSION BC066260
VERSION BC066260.1 GI:42542587
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

DS^a
LKRKPSTNAGRQKRLTQPCSDSYEKPPKEFLERFKSLQKMIHQHLSRTHGSE

AGAGTGTGTCGCTTTCTCCTGTTTCAGAAAGCCAGCTGAATCGCAACACC 183

AAATGAAGGATAATCAATGTATCAATTAAAAAGCTGAAGAGGAAACCACTTCC 372

CCGCCGAAGAATTCTGGAACGTTCAATCCCTGCGAGAAATGATTAC 363

566 bp mRNA linear PRI 08-MAR-2005
 cdns interleukin 21, mRNA (cDNA clone MGC:79376
 71861), complete cds.

; Eutheria; Euarchontoglires; Primates; Catarrhini;

JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J,

as 1 to 566)

AUTHORS
 Director MGC Project.
TITLE
 Direct Submission
JOURNAL
 Submitted (03-FEB-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Narayan Bhat
 CDNA Library Preparation: Bhat Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 172 Row: d Column: 20
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 11141874.

FEATURES
 source
 1..566
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="MGC:79376 IMAGE:6971861"
 /rissue_type="PCR rescued clones"
 /clone_id="NIH_MGC_195"
 /lab_host="DH10B"
 /note="Vector: pDNR-Dual1"
 1..566
 /gene="IL21"
 /note="Synonyms: Zall, IL-21"
 /db_xref="GeneID:59067"
 /db_xref="MIM:605384"
 46..534
 /gene="IL21"
 /codon_start=1
 /product="interleukin 21"
 /protein_id="AAH66258.1"
 /db_xref="GI:42542659"
 /db_xref="GeneID:59067"
 /db_xref="MIM:605384"
 /translation="MRSSPGMERIVICLMTVPLGLTVHKSQGDPMIRMOILIDIVDQKTVNDLVPFELPAPEDVETNCMSAFSCFOKQLKSANTGNERRILINISIKLKRKPPSTNAGRORHRLTCCPSCDSEKPKPEFLERKSLLOKMIHQHLSRTGSEDS"
 ORIGIN
 Query Match 74.0%; Score 299.6; DB 5; Length 566;
 Best Local Similarity 84.1%; Pred. No. 3.8e-92;
 Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

4 CAAGGTCAAGATCGGCACATGATTTGAATGCGTCACTTATGATATTGTCATCAGCTG 63
 Db 133 CAAGGTCAAGATCGGCACATGATTTGAATGCGTCACTTATGATATTGTCATCAGCTG 192
 Qy 64 AAAAATTAATGATGATGACCTGCTTCCGGAATTCCTCGCGCTCCGGAAGATGTTGAGACC 123
 Db 193 AAAAATTAATGATGATGACCTGCTTCCGGAATTCCTCGCGCTCCGGAAGATGTTGAGACC 252
 Qy 124 AACTGTGATGATGATGACCTGCTTCCGGAATTCCTCGCGCTCCGGAAGATGTTGAGACC 183
 Db 253 AACTGTGATGATGATGACCTGCTTCCGGAATTCCTCGCGCTCCGGAAGATGTTGAGACC 312
 Qy 184 GGTAAACAAGAACGATCATCAAGCTTCCATTAAAAAAGCTAAACGCTAAACGCGCTCC 243
 Db 313 GGAACAATGAAGATTAATCAATGATTAATTAAGAGGAGGAGAAACCACTTCC 372

Qy 244 ACCAAGCAGGATCGTCTGACAGAAACACCGCTGACCTGCCGCTGTGATTTATGATGAG 303
 Db 373 ACAATTCAGGAGAGAGACAGAAACACGACTTAACATCCCTTATGATTTATGATGAG 432
 Qy 304 AAAAAACCGCGAAAGAAATTCCTGGAACGTTTCAAAATCCCTGTCGAGAAAAATGATTCAC 363
 Db 493 AAAAAACCGCGAAAGAAATTCCTGGAACGTTTCAAAATCCCTGTCGAGAAAAATGATTCAT 492
 Qy 364 CAGCATCTGTCTCTCTGATCCACGAGCTTCGGAAGATTTCTGA 405
 Db 493 CAGCATCTGTCTCTCTGATCCACGAGCTTCGGAAGATTTCTGA 534

RESULT 8
 LOCUS
 DEFINITION
 Homo sapiens interleukin 21, mRNA (CDNA clone MGC:79379 IMAGE:6971865), complete cds.
 ACCESSION
 BC066261
 VERSION
 BC066261.1 GI:42542656
 KEYWORDS
 MGC.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 566)
 Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD, Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T, Max SI, Wang J, Hsieh F, Diatchenko L, Manisina K, Farmer AA, Rubin GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL, Scheetz TE, Brownstein MJ, Ucdin TB, Toshiyuki S, Carninci P, Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy SJ, Bosc SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH, Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SM, Villalón DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J, Helton E, Kettelman M, Madan A, Rodriguez S, Sanchez A, Whitting M, Madan A, Young AC, Shevchenko Y, Boultard G, Blakeley RW, Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J, Schmutz J, Myers RM, Butlerfield JS, Krzywinski M, Skalska U, Smalusz DE, Scherch A, Schein JE, Jones SJ and Marra MA.
 Mammalian Gene Collection Program Team
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 2 (bases 1 to 566)
 Director MGC Project.
REFERENCE
 JOURNAL
 PUBMED
 TITLE
 DIRECTOR MGC PROJECT.
REFERENCE
 JOURNAL
 Submitted (03-FEB-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Narayan Bhat
 CDNA Library Preparation: Bhat Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 172 Row: d Column: 16
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 11141874.
 Location/Qualifiers


```

source
1..566
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:79379 IMAGE:6971865"
/issue_type="PCR rescued clones"
/clone_id="NIH_MGC_195"
/lab_host="DH10B"
/notes="Vector: pDNR-Dual"
1..566
gene
/clone="IL21"
/notes="synonyms: Zall, IL-21"
/db_xref="GeneID:59067"
/db_xref="MIM:605384"
46..534
CDS
/clone="IL21"
/codon_start=1
/product="interleukin 21"
/protein_id="AAH6262.1"
/db_xref="GI:42542807"
/db_xref="GeneID:59067"
/db_xref="MIM:605384"
/translation="MRSSPGNMRIVICLVIFLGLVHKSSQGGDRHNIIRNQLID
IVOLKNYVDLVEFLPAPEDVETNEMAFSCFOCAQKSNANTGNNEIIVSIRK
LKKRPSTNAGRGQRHLTCPCSDSYEKPKPFLERFKSLQKMHQHLSPRTGSE
DS"
ORIGIN
Query Match 74.0%; Score 299.6; DB 5; Length 566;
Best Local Similarity 84.1%; Pred. No. 3.8e-92;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 4 CAAGGTAAAGTCCCAATGATTAAGTGAATGCTCACTTATAGTATTTGATGACAGT 63
Db 133 CAAGGTAAAGTCCCAATGATTAAGTGAATGCTCACTTATAGTATTTGATGACAGT 192
QY 64 AAAAATATGTAATGACCTGTTCCGGAATTCCTGCGGCTCGGAAGATGTGAGACC 123
Db 193 AAAAATATGTAATGACCTGTTCCGGAATTCCTGCGGCTCGGAAGATGTGAGACC 252
QY 124 AACTGTAGTGTCCGCTTCTCCTGTTCCAGAAAGCCAGCTGAATCCGCAACACC 183
Db 253 AACTGTAGTGTCCGCTTCTCCTGTTCCAGAAAGCCAGCTGAATCCGCAACACC 312
QY 184 GGTACACGAACTATCATCAAGTTCCATTAAAACTGAAACCTGAACCGCCGCTCC 243
Db 313 GGAACCATGAAGATATCAATGATCAATTAAGCTGAAGAGCAACCACTTCC 372
QY 244 ACCAAGCAGGTGCTGTCAGAAACCGTCTGACGCTCCGCTGATTTATGAG 303
Db 373 ACCAATGAGGAGAGACAGAAACCACTTAACATGCTTATGATTTATGAG 432
QY 304 AAAAACCAGCGAAAGATTCCTGGAACGTTTCAATCCCTGTCAGAAATGATTCAC 363
Db 433 AAAAACCAGCGAAAGATTCCTGGAACGTTTCAATCCCTGTCAGAAATGATTCAC 492
QY 364 CAGCACTGTCTCTGTTACCAAGGTTCCGAAGATTCCTGA 405
Db 493 CAGCATCTGTCTCTGTTACCAAGGTTCCGAAGATTCCTGA 534

RESULT 9
LOCUS BC066262 566 bp mRNA linear PRI 08-MAR-2005
DEFINITION Homo sapiens interleukin 21, mRNA (CDNA clone MGC:79380
IMAGE:6971866), complete cds.
ACCESSION BC066262
VERSION BC066262.1 GI:42542806
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

```

```

REFERENCE
AUTHORS
Hominidae; Homo.
1 (bases 1 to 566)
Straussberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD,
Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg
B, Bietow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T,
Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin
GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL,
Scheltz TE, Brownstein MJ, Udell TB, Toshiyuki S, Carninci P,
Prange C, Raha S, Loquellano NA, Peters CJ, Abramson RD, Mullianhy
SU, Bosak SA, McEwan PJ, McKernan KJ, Hale S, Garcia AM, Gay LJ, Hulik SW,
Villalón DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J,
Helton B, Kettelman M, Madan A, Rodriguez S, Sanchez A, Whiting M,
Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW,
Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J,
Schmutz J, Myers RM, Butlerfield JS, Krzyzinski MI, Skalska U,
Smalilus DE, Schnerker A, Schein JE, Jones SJ and Marra MA.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 566)
REFERENCE
DIRECTOR MGC Project.
DIRECT SUBMISSION
Submitted (03-FEB-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: gcgaps-remail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Bhat Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
Series: IRAK Plate: 172 Row: d Column: 15
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 1141874.
1..566
FEATURES
source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:79380 IMAGE:6971866"
/issue_type="PCR rescued clones"
/clone_id="NIH_MGC_195"
/lab_host="DH10B"
/notes="Vector: pDNR-Dual"
1..566
gene
/clone="IL21"
/notes="synonyms: Zall, IL-21"
/db_xref="GeneID:59067"
/db_xref="MIM:605384"
46..534
CDS
/clone="IL21"
/codon_start=1
/product="interleukin 21"
/protein_id="AAH6262.1"
/db_xref="GI:42542807"
/db_xref="GeneID:59067"
/db_xref="MIM:605384"
/translation="MRSSPGNMRIVICLVIFLGLVHKSSQGGDRHNIIRNQLID
IVOLKNYVDLVEFLPAPEDVETNEMAFSCFOCAQKSNANTGNNEIIVSIRK
LKKRPSTNAGRGQRHLTCPCSDSYEKPKPFLERFKSLQKMHQHLSPRTGSE
DS"

```


ORIGIN DS"

Query Match 74.0%; Score 299.6; DB 5; Length 566;
Best Local Similarity 84.1%; Pred. No. 3.8e-92;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 4 CAAGTCAGATGCGACATGATTTGAATGCGTCAACTTATGATATTGTTGATCAGCTG 63
DB 133 CAAGTCAGATGCGACATGATTTGAATGCGTCAACTTATGATATTGTTGATCAGCTG 192
QY 64 AAAAATTATGTAATGATGACCTGGTCCGGAATTCCTGCGGCTCCGGAAGATTGAGACC 123
DB 193 AAAAATTATGTAATGATGACCTGGTCCGGAATTCCTGCGGCTCCGGAAGATTGAGACA 252
QY 124 AACTGTGATGTCGCTGCTTCTCTGCTTTCCAGAAAGCCGACGTGAATCCGCAAAACC 183
DB 253 AACTGTGATGTCGCTGCTTCTCTGCTTTCCAGAAAGCCGACGTGAATCCGCAAAATCA 312
QY 184 GGTACACAGAACGATATCATCACTTTCCATTAAAAAAGTAAACGTTAAACCGCGTCC 243
DB 313 GGAACCAATGAAAGATATCAATGATCAATTAAGCTGAAGAGAACCAACCTTCC 372
QY 244 ACCAAGCAGGTCGTCTGACAAACACCGTCTGACCTGCTGCTGATTTCTATGAG 303
DB 373 ACAATTCAGGAGAGAGACAGAAACACAGACTTAACATGCTTCAATGATTTCTATGAG 432
QY 304 AAAAAACCCGGAAGAAATTCCTGGAACGTTCAATCCCTGCTGCAGAAATGATTCAC 363
DB 433 AAAAAACCAACCAAGAAATTCCTTAAGAAATTCCTTAAGAAATGATTCAT 492
QY 364 CAGCACCTGCTCTCTGTAACCCAGCGTTCCGAAGTTCTCTGA 405
DB 493 CAGCATCTGCTCTTGAACACACGGAAGTGAATCTCTGA 534

RESULT 10
AR174547 642 bp DNA linear PAT 17-DEC-2001
LOCUS AR174547 Sequence 1 from patent US 6307024.
DEFINITION AR174547
ACCESSION AR174547
VERSION AR174547.1 GI:17914867
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 642)
AUTHORS Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D., Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and Hammond,A.K.
TITLE Cytokine zalphal1 ligand
JOURNAL Patent: US 6307024-A 1 23-OCT-2001;
FEATURES
source 1. 642
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 74.0%; Score 299.6; DB 2; Length 642;
Best Local Similarity 84.1%; Pred. No. 4e-92;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 4 CAAGTCAGATGCGACATGATTTGAATGCGTCAACTTATGATATTGTTGATCAGCTG 63
DB 134 CAAGTCAGATGCGACATGATTTGAATGCGTCAACTTATGATATTGTTGATCAGCTG 193
QY 64 AAAAATTATGTAATGATGACCTGGTCCGGAATTCCTGCGGCTCCGGAAGATTGAGACC 123
DB 194 AAAAATTATGTAATGATGACCTGGTCCGGAATTCCTGCGGCTCCGGAAGATTGAGACA 253
QY 124 AACTGTGATGTCGCTGCTTCTCTGCTTTCCAGAAAGCCGACGTGAATCCGCAAAACC 183
DB 254 AACTGTGATGTCGCTGCTTCTCTGCTTTCCAGAAAGCCGACGTGAATCCGCAAAATCA 313

QY 184 GGTACACAGAACGATATCATCACTTTCCATTAAAAAAGTAAACGTTAAACCGCGCTCC 243
DB 314 GGAACCAATGAAAGATATCAATGATCAATTAAGCTGAAGAGAACCAACCTTCC 373
QY 244 ACCAAGCAGGTCGTCTGACAAACACCGTCTGACCTGCTGCTGATTTCTATGAG 303
DB 374 ACAATTCAGGAGAGAGACAGAAACACAGACTTAACATGCTTCAATGATTTCTATGAG 433
QY 304 AAAAAACCCGGAAGAAATTCCTGGAACGTTCAATCCCTGCTGCAGAAATGATTCAC 363
DB 434 AAAAAACCAACCAAGAAATTCCTTAAGAAATTCCTTAAGAAATGATTCAT 493
QY 364 CAGCACCTGCTCTCTGTAACCCAGCGTTCCGAAGTTCTCTGA 405
DB 494 CAGCATCTGCTCTTGAACACACGGAAGTGAATCTCTGA 535

RESULT 11
BD248940 642 bp DNA linear PAT 17-JUL-2003
LOCUS BD248940 Novel cytokine ZALPHA11 ligand.
DEFINITION BD248940
ACCESSION BD248940.1 GI:33058710
VERSION JP 2002537839-A/1.
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 642)
AUTHORS Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D., Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and Hammond,A.K.
TITLE Novel cytokine ZALPHA11 ligand
JOURNAL Patent: JP 2002537839-A 1 12-NOV-2002;
COMMENT
OS Homo sapiens (human)
PN JP 2002537839-A/1
PD 12-NOV-2002
PF 09-MAR-2000 JP 2000603382
PR 09-MAR-1999 US 09/264908, 11-MAR-1999 US 09/265992 PR 01-JUL-1999 US 60/142013
PI JULIA E NOVAK, SCOTT R PRESNELL, CINDY A SPEECHER, DONALD C PI FOSTER,
PI RICHARD D HOLLY, JANE A GROSS, JANET V JOHNSTON, ANDREW J NELSON,
PI STACEY R DILLON, ANGELA K HAMMOND
PC C12N15/09,A61K38/00,A61P35/00,A61P37/00,C07K14/52,
PC C07K14/53,
PC C07K14/54,C07K14/55,C07K16/24,C07K19/00,C12N1/15,C12N1/19, PC C12N1/21,
PC C12N5/10,C12P21/02,C12P21/02,G01N33/53,C12N15/00,C12N5/00, PC A61K37/02
CC Novel cytokine ZALPHA11 ligand
FH Key Location/Qualifiers
FT CDS Location/Qualifiers
1. 642
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 74.0%; Score 299.6; DB 2; Length 642;
Best Local Similarity 84.1%; Pred. No. 4e-92;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 4 CAAGTCAGATGCGACATGATTTGAATGCGTCAACTTATGATATTGTTGATCAGCTG 63
DB 134 CAAGTCAGATGCGACATGATTTGAATGCGTCAACTTATGATATTGTTGATCAGCTG 193
QY 64 AAAAATTATGTAATGATGACCTGGTCCGGAATTCCTGCGGCTCCGGAAGATTGAGACC 123

Db	194	AAAAATTATGTGAATGACTTGTTGGCTGTAATTTCTGCGACGCTCCAGAAAGATGTAGAGCA	255
Qy	124	AACGTGAGTGTGTCGGCTTTCTCTCTGTTTCCAGAAAGCCGACGCTGAATTCGGCAACACC	183
Db	254	AACGTGAGTGTGACTTTTCTCTGTTTCCAGAAAGCCCAACTAAAGTCAGCAAAATACA	313
Qy	184	GGTAAACAAGAACGATCATCAAGCTTTCATTAAAAACGAAACGTAACCGCGCTCC	243
Db	314	GGAACCAATGAAAGGATTAATCAATGTATCAATTAAGAGCTGAAGAGGAAACCACTTCC	373
Qy	244	ACCAACGAGGTGCTGTCAGAAAACCCGCTGACCTGCGCTGCTGATCTTATGAG	303
Db	374	ACAATGACAGGGAAGAGACAGAAACAGACTAACATGATCCCTTATGATTTCTTAAG	433
Qy	304	AAAAAACCCCGAAAGAATTCCTGGAACGTTTCAATTCCTGCTGACAGAAATGATTAC	363
Db	434	AAAAAACCAACCAAGAATTCCTGAAAGATTCAAATCATCTTCCAAAAATGATTCAT	493
Qy	364	CAGCACCTGTCTCTCGTACCAAGGTTCCGAAGATTCCTGA	405
Db	494	CAGCATCTGTCTCTTGAACAACAAGGAAGTGAAGTCTCTGA	535
RESULT 12			
LOCUS	CS034091	642 bp	DNA linear PAT 10-MAR-2005
DEFINITION	Sequence 3597 from Patent WO2005016962.		
ACCESSION	CS034091		
VERSION	CS034091.1	GI:60732828	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens (human)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.		
AUTHORS	1		
TITLE	Abbas, A.; Clark, H., Ouyang, W., Williams, M.P., Wood, W. I. and Wu, T.D.		
JOURNAL	Compositions and methods for the treatment of immune related diseases		
FEATURES	Patent: WO 2005016962-A 3597 24-FEB-2005; Genentech, Inc. (US)		
SOURCE	location/Qualifiers		
ORIGIN	1..642		
	/organism="Homo sapiens"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:9606"		
Query Match	74.0%; Score 299.6; DB 2; Length 642;		
Best Local Similarity	84.1%; Pred. No. 4e-92;		
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;			

Db	434	AAAAAACCCACCAAGATTCTCTAGAAAGATTCAAAATCACTTCCAAAAAGATGATTCAT	493
Qy	364	CAGCACTGTCTCTCGTACCCAGGTTCCGAGATTCCTGA	405
Db	494	CAGCATCTGTCTCTAGAACACACGGAAGTGAATTCCTGA	535
RESULT 13			
LOCUS	CS036718	642 bp	DNA
DEFINITION	Sequence 6224 from Patent WO2005016962.	linear	PAT 10-MAR-2005
ACCESSION	CS036718		
VERSION	CS036718.1	GI:60734171	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
AUTHORS	Homo sapiens		
TITLE	Mamalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eumariota; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.		
JOURNAL	Abbas, A., Clark, H., Ouyang, W., Williams, M. P., Wood, W. I. and Wu, T. D. Compositions and methods for the treatment of immune related diseases		
FEATURES	Patent: WO 2005016962-A 6224 24-FEB-2005; Genentech, Inc. (US)		
source	Location/Qualifiers 1..642 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"		
ORIGIN			
Query Match	74.0%; Score 299.6; DB 2; Length 642;		
Best Local Similarity	84.1%; Pred. No. 4e-92;		
Matches	338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;		
Qy	4	CAAGTCAAAGTCCGCACATGATTAGAAATGGTCAACTTATAGTATTTGATCAGCTG	63
Db	134	CAAGGTCAAGATCCCACTGATGATTAAGATGGTCAACTTATAGATTTGATCAGCTG	193
Qy	64	AAAAATTATGAAAGACCTGGTCCGGAAATTCCTGCGGGCTCCGAAAGATGTGAGACC	123
Db	194	AAAAATTATGAAATGACTTGGTCCCTGGAATTTCTCCAGCTCCAGAAAGATGTAGACCA	253
Qy	124	AACGTGAGTGGTCCGCTTTTCTCTGTTTCCAGAAAGCCAGCTGAATTCGCAAAACACC	183
Db	254	AACGTGAGTGGTCCGCTTTTCTCTGTTTCCAGAAAGCCCAACTGAAGTCAAGAAATCA	313
Qy	184	GCTAACACGACGTATCATCAGTTTCCATTAAAAAAGTGAAGCTGAAGCCGCTCC	243
Db	314	GGAACAAATGAAAGATATCAATGATCAATTTAAAAAGCTGAAGAGAAACCACTTCC	373
Qy	244	ACCAACGAGGTGCTGTCGACAGAAACACGCTGACCTGCCGCTGCTGATTTCTTAGAG	303
Db	374	ACAAATGAGGGAAGAGACACAGAAACACAGACTTAACATGCTTATATGATTTCTTAGAG	433
Qy	304	AAAAAACCGCGGAAGAATTCCTGGAACGTTTCAATTCCTGCTGCAGAAAAATGATTCAC	363
Db	434	AAAAAACCAACCAAGAATTCCTGGAAGAATTCCTGGAAGAATTCCTGCAAAAAATGATTCAT	493
Qy	364	CAGCACTGTCTCTCGTACCCAGGTTCCGAGATTCCTGA	405
Db	494	CAGCATCTGTCTCTAGAACACACGGAAGTGAATTCCTGA	535
RESULT 14			
LOCUS	CS043043	642 bp	DNA
DEFINITION	Sequence 3597 from Patent WO2005019258.	linear	PAT 22-MAR-2005
ACCESSION	CS043043		
VERSION	CS043043.1	GI:61850089	
KEYWORDS			

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Euteria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 Abbas, A., Clark, H., Ouyang, W., Williams, P.M., Wood, W.I. and Wu, T.D.
TITLE	Compositions and methods for the treatment of immune related diseases
JOURNAL	Patent: WO 2005019258-A 3597 03-MAR-2005; Genentech, Inc. (US)
FEATURES	location/Qualifiers
source	1..642 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
ORIGIN	
Query Match	74.0%; Score 299.6; DB 2; Length 642;
Best Local Similarity	84.1%; Pred. No. 4e-92;
Matches 338; Conservative	0; Mismatches 64; Indels 0; Gaps 0;
Qy	4 CAAGGTCAAGATCGGCACATGATTTGAATGCGTCAACTATATGATTTGTTGATGAGCTG 63
Db	134 CAGGTCAAGATCGGCACATGATTTGAATGCGTCAACTATATGATTTGTTGATGAGCTG 193
Qy	64 AAAAAATTATGTGAATGACCTGGTTCCGGAAATTCCTCGCGGCTCCGGAAAGATGTGAGACC 123
Db	194 AAAAAATTATGTGAATGACCTGGTTCCGGAAATTCCTCGCGGCTCCGGAAAGATGTGAGACC 253
Qy	124 AACTGTGAGTGTCCGCTTTTCTCTGTTTCCAGAAAGCCAGCTGAAATCCGCAAAACCC 183
Db	254 AACTGTGAGTGTCTGCTTTTCTCTGTTTCCAGAAAGCCCACTAAAGTCAGCAATATCA 313
Qy	184 GGTAAACAAGACGATATCATCAAGCTTCCATTAAAAAATGAAACGTAAACCGCCGCC 243
Db	314 GGAACAATGAAAGATTAATCATATTAATTAATTAAGCTGAAGAGAAACCAACCTTCC 373
Qy	244 ACCAAGCAGAGTCTGTCGTAGAAACACCGCTGACCTGCCGCTCTGTGATTTCTTAAG 303
Db	374 ACAATGACAGGAGAAAGACAGAAACACAGACATATCCCTTATGATTTCTTAAG 433
Qy	304 AAAAAACCGCGAAAGAAATTCCTGGAAGCTTCAAAATCCTGCTGCAAGAAATGATTAC 363
Db	434 AAAAAACCAACCAAGAAATTCCTGGAAGAAATGCAATCACTTCCAAAAGATGATTCAT 493
Qy	364 CAGCACCTGCTCTCTCTGTAACCAAGCGTTCCAGAAATTTCTGA 405
Db	494 CAGCATCTGCTCTCTGTAACCAAGCGAAAGTGAAGATTTCTGA 535
RESULT 15	
LOCUS	CS045670 642 bp DNA linear PAT 22-MAR-2005
DEFINITION	Sequence 6224 from Patent WO2005019258.
VERSION	CS045670
KEYWORDS	CS045670.1 GI:61851968
SOURCE	
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Euteria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
TITLE	1 Abbas, A., Clark, H., Ouyang, W., Williams, P.M., Wood, W.I. and Wu, T.D.
JOURNAL	Compositions and methods for the treatment of immune related diseases
FEATURES	Patent: WO 2005019258-A 6224 03-MAR-2005; Genentech, Inc. (US)
source	location/Qualifiers
	1..642 /organism="Homo sapiens" /mol_type="unassigned DNA"

```

ORIGIN
/db_xref="taxon:9606"

Query Match      74.0%; Score 299.6; DB 2; Length 642;
Best Local Similarity 84.1%; Pred. No. 4e-92;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0

QY      4 CAAGTCAGATCCGCACATGATTGAAATGCGTCACTTATGATATTTGTTGATCACTG 63
DB      134 CAAGTCAGATCCGCACATGATTGAAATGCGTCACTTATGATATTTGTTGATCACTG 193

QY      64 AAAAAATTATGTGAATGACCTGTTCCGGAATTTCCGCCGGCTCCGGAAGATGTTGAGAC 123
DB      194 AAAAAATTATGTGAATGACCTGTTCCCTGAATTTCTGCCAGCTCCGGAAGATGTTAGACA 253

QY      124 AACTGTAGTGTGCTCCGCTTCCGTTCCGTTCCAGAAAGCCCACTGAATTCGCAACACC 183
DB      254 AACTGTAGTGTGCTCCGCTTCCGTTCCGTTCCAGAAAGCCCACTGAATTCGCAACAAATACA 313

QY      184 GGTAAACAAGACGATCATCAACGTTTCCATTAAAAAAGTAAGTAACCGCCGCTCC 243
DB      314 GGAACCAATGAAGGATATATCAATGTATCAATTAAAGGCTGAAGAGAAACCACTTCC 373

QY      244 ACCAAGCAGGTCGTCGTCAAGAAACACCGCTGACCTGCCGCTCGTGATTTCTTATAG 303
DB      374 ACAATGTAGGAGAAAGACAGAAACACAGACTTAAATATGCCCTTATGTGATTTCTTATAG 433

QY      304 AAAAAACCGCGAAAGAAATTCCTGAAACGTTTCAATCCCTGCTGCAGAAAAATGATTAC 363
DB      434 AAAAAACCAACCAAGAAATTCCTGAAAGAAATTCCAATCACTTCTCCAAAAAGATGATTAT 493

QY      364 CAGCACTGTCTCTCTGTAACCAACGTTCCGAAGTTCTCTGA 405
DB      494 CAGCATGTCTCTCTAGAACACACGGAAGTGAAGTCTCTGA 535

```

THIS PAGE LEFT BLANK

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2006, 12:03:41 ; Search time 520 Seconds

(without alignments)
5430.309 Million cell updates/sec

Title: US-10-735-149-27

Perfect score: 405
Sequence: 1 atgcaagctcaagatcgcca.....acggctccgaagattcctga 405

Scoring table: IDENTITY_NUC
Gap 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseqn1980s:*
1: geneseqn1980s:*
2: geneseqn1980s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	405	100.0	405	12	ADP70484
2	299.6	74.0	483	6	AAS20695
3	299.6	74.0	483	10	ADH44633
4	299.6	74.0	483	10	ADH44633
5	299.6	74.0	483	12	ADP19792
6	299.6	74.0	483	12	ADP19792
7	299.6	74.0	483	14	ADV96416
8	299.6	74.0	489	10	ADP17040
9	299.6	74.0	489	14	ADV42801
10	299.6	74.0	642	3	AAAS75552
11	299.6	74.0	642	6	AAAS20637
12	299.6	74.0	642	9	AAAD47852
13	299.6	74.0	642	10	ADH44571
14	299.6	74.0	642	10	ADH44571
15	299.6	74.0	642	12	ADH10500
16	299.6	74.0	642	12	ADP10556
17	299.6	74.0	642	12	ADP19730
18	299.6	74.0	642	12	ADP70458

19	299.6	74.0	642	14	ADV96354	ADV96354 Human zal
20	299.6	74.0	642	14	ADY20418	ADY20418 DNA encod
21	299.6	74.0	642	14	ADY17791	ADY17791 DNA encod
22	299.6	74.0	642	14	ADZ20500	ADZ20500 DNA encod
23	299.6	74.0	642	14	AED68670	AED68670 Human int
24	298	73.6	489	12	ADMA1018	ADMA1018 Human IL-
25	298	73.6	489	12	AEB26427	AEB26427 CDNA enco
26	298	73.6	611	15	AEB74873	AEB74873 Human IL-
27	298	73.6	617	8	ACC80873	ACC80873 Human IL-
28	298	73.6	617	9	ACD26729	ACD26729 CDNA enco
29	298	73.6	617	12	ADJ25620	ADJ25620 Human int
30	298	73.6	617	13	ADSL9022	ADSL9022 Human int
31	298	73.6	617	15	AEB19671	AEB19671 Human int
32	298	73.6	617	15	AEG05272	AEG05272 Human IL-
33	296.6	73.2	399	14	ADH43686	ADH43686 DNA encod
34	296.6	73.2	486	6	ADZ22923	ADZ22923 Human BOL
35	294.8	72.8	489	9	AAAD47854	AAAD47854 Human int
36	293.6	72.5	1560	3	AAAS75599	AAAS75599 Nucleotid
37	293.6	72.5	1560	6	AAAS20714	AAAS20714 DNA encod
38	293.6	72.5	1560	10	ADH44654	ADH44654 Human zal
39	293.6	72.5	1560	10	ADH44654	ADH44654 Human zal
40	293.6	72.5	1560	12	ADP19813	ADP19813 Human zal
41	293.6	72.5	1560	14	ADV96437	ADV96437 Human zal
42	291.6	72.0	642	13	ADY27248	ADY27248 Human int
43	290.6	71.8	486	3	AAAS75553	AAAS75553 Dengenera
44	290.6	71.8	486	6	AAS20638	AAS20638 Dengenera
45	290.6	71.8	486	10	ADH44573	ADH44573 Degenerat

ALIGNMENTS

RESULT 1
ID ADP70484
ADP70484 standard; cDNA; 405 BP.
XX
AC ADP70484;
XX
DT 23-SEP-2004 (first entry)
XX
DE Codon optimised interleukin 21 (IL-21) encoding cDNA SEQ ID NO:27.
XX
KM interleukin 21; IL-21; human; gene; ss; codon optimised.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1..405
FT /tag= a
FT /product= "interleukin 21 (IL-21)"
XX
PN W02004055168-A2.
XX
PD 01-JUL-2004.
XX
PF 12-DEC-2003; 2003WO-US039764.
XX
PR 13-DEC-2002; 2002US-0433448P.
XX
RR 13-DEC-2002; 2002US-0433452P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Chang C, Zamost BL, Covert DC, Liu HY, De Jongh KS, Meyer JD;
XX
DR Holderman SD;
XX
WP1; 2004-500211/47.
XX
P-PSDB; ADP70485.
XX
PT New expression vectors for the large-scale production of IL-21 proteins
XX
PT comprises a prokaryotic origin of replication, a transcriptional
XX
PT initiation DNA element, a polynucleotide sequence and a transcriptional
XX
PT terminator.

RESULT 3
ADH44633
ID ADH44633 standard; DNA; 483 BP.
XX
AC ADH44633;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human Zalphall ligand cDNA fragment.
XX
KW Human; ss; Zalphall1 ligand; Zalphall1 receptor; immune response;
KW tumour progression; metastasis; tumour stasis; haematopoietic tumour;
KW lymphoma; B cell tumour; systemic lupus erythematosus;
KW rheumatoid arthritis; myasthenia gravis; diabetes; infectious disease;
KW immunocompromised patient; HIV infection; vaccine; chromosome 4q27.
XX
OS Homo sapiens.
XX
PN US6605272-B2.
XX
PD 12-AUG-2003.
XX
PE 03-AUG-2001; 2001US-00923246.
XX
PR 09-MAR-1999; 99US-0123547P.
PR 11-MAR-1999; 99US-0123904P.
PR 01-JUL-1999; 99US-0142013P.
PR 09-MAR-2000; 2000US-00522217.
XX
XX (ZYMO) ZYMOGENETICS INC.
PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
PI Gross JA, Johnson JV, Nelson AJ, Dillon SR, Hammond AK;
XX
XX WPI: 2003-895283/82.
XX
PT Stimulating an immune response in a mammal exposed to an antigen or
PT pathogen, useful for enhancing anti-tumor activity resulting in reduced
PT tumor progression or metastasis, comprises administering zalphall1 ligand
PT polypeptide.
XX
XX Example 25; SEQ ID NO 63; 103bp; English.
XX
XX The invention relates to stimulating an immune response in a mammal
XX exposed to an antigen or pathogen comprising administering a composition
XX comprising mature zalphall1 ligand polypeptide comprising residues 32-162
XX of ADH44633 in a pharmaceutical vehicle. Also included are stimulating an
XX immune response in a mammal exposed to an antigen or pathogen
XX (comprising: (a) determining (in)directly the level of antigen or
XX pathogen present in the mammal; (b) administering a composition
XX comprising zalphall1 ligand polypeptide in a pharmaceutical vehicle; (c)
XX determining (in)directly the level of antigen or pathogen in the mammal;
XX and (d) comparing the antigen or pathogen level in (a) with (b), where a
XX change in the level indicates stimulation of immune response), and
XX stimulating an immune response in a mammal exposed to an antigen or
XX pathogen (comprising: (a) determining a level of antigen- or pathogen-
XX specific antibody; (b) administering a composition comprising zalphall1
XX ligand polypeptide in a pharmaceutical vehicle; (c) determining a post
XX administration level of the antigen- or pathogen-specific antibody; and
XX (d) comparing the level of the antibody in (a) with (b), where an
XX increase in the antibody level indicates stimulation of immune response).
XX The method is useful for stimulating an immune response in a mammal
XX exposed to an antigen or pathogen, and for enhancing anti-tumor activity
XX resulting in a reduction in tumor progression, decrease in metastasis,
XX or tumour stasis. The tumour may be a haematopoietic tumour, a lymphoma
XX or a B cell tumour. The zalphall1 ligand is useful for treating a wide
XX range of diseases arising from defects in the immune system, e.g.
XX systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis, or
XX diabetes, for boosting immunity to infectious diseases, treating
XX immunocompromised patients, such as HIV+ patients and in improving
XX vaccines. The present sequence is a human Zalphall1 ligand cDNA (or

CC Fragment).
XX
SQ Sequence 483 BP; 167 A; 103 C; 96 G; 117 T; 0 U; 0 Other;
XX
Query Match 74.0%; Score 299.6; DB 10; Length 483;
Best Local Similarity 84.1%; Pred. No. 1.3e-83;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
QY 4 CAAGTCAAGATCCGACATGATTGAAATGCGTCACTTATGATATTGTCATGCTG 63
DB 82 CAAGTCAAGATCCGACATGATTGAAATGCGTCACTTATGATATTGTCATGCTG 141
QY 64 AAAAATTATGAAAGACCTGTTCCGGAATTCGCGCGGTCGGGAAGATGTGAGACC 123
DB 142 AAAAATTATGAAAGACCTGTTCCGGAATTCGCGCGGTCGGGAAGATGTGAGACA 201
QY 124 AACTGTGAGTGTCCGCTTTCTCTGTTTCCAGAAAGCCAGCTGAAAATCCGCAACACC 183
DB 202 AACTGTGAGTGTCCGCTTTCTCTGTTTCCAGAAAGCCAGCTGAAAATCCGCAACACC 261
QY 184 GGTAAACAAGACGTATCATCAACGTTTCCATTAAAAAAGTAAACGCGCTCC 243
DB 262 GAAATCAATGAAGATATATCAATGTATCAATTAAGCTGAAGAGAAACCACTTCC 321
QY 244 ACCAAGCAGTGTCTGTCAGAAAACCGTCTGACCTGCGCTCTGTCATTCTATGAG 303
DB 322 ACAAATGACAGGAGAAACAGAAACAGACATCAATGCTTCAATGATTTATGAG 381
QY 304 AAAAATCCGCGAAGAAATTCCTGGAAGCTTCAATCCCTGCTCAGAAAATGATTCAC 363
DB 382 AAAAATCCGCGAAGAAATTCCTGGAAGCTTCAATCCCTGCTCAGAAAATGATTCAT 441
QY 364 CAGCAGTGTCTCTCTGTCAGAACCGTTCGGAAGATTCCTGA 405
DB 442 CAGCAGTGTCTCTCTGTCAGAACCGTTCGGAAGATTCCTGA 483
RESULT 4
AD100969
ID AD100969 standard; cDNA; 483 BP.
XX
AC AD100969;
XX
DT 22-APR-2004 (first entry)
XX
DE Human zalphall1 ligand cDNA fragment - SEQ ID 63.
XX
KW zalphall1 ligand; immunity; infectious disease; immunocompromised patient;
KW HIV; vaccine; human; ss.
XX
OS Homo sapiens.
XX
PN US2003125524-A1.
XX
PD 03-JUL-2003.
XX
PE 15-NOV-2002; 2002US-00295723.
XX
PR 09-MAR-2000; 2000US-00522217.
XX
XX (ZYMO) ZYMOGENETICS INC.
PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
PI Gross JA, Johnson JV, Nelson AJ, Dillon SR, Hammond AK;
XX
XX WPI: 2003-811003/76.
XX
XX New zalphall1 ligand polypeptides, useful for boosting immunity to
XX infectious diseases, and creating immunocompromised patients, such as
XX human immunodeficiency virus (HIV) patients, or in improving vaccines.
XX
XX Example 25; SEQ ID NO 63; 113bp; English.
XX

CC The invention relates to a novel isolated zalphall ligand polypeptide.
CC The polypeptide of the invention may be useful for boosting immunity to
CC infectious diseases and treating immunocompromised patients, such as HIV
CC patients, as well as in improving vaccines. The current sequence is that
CC of the human zalphall ligand cDNA fragment of the invention.

XX Sequence 483 BP; 167 A; 103 C; 96 G; 117 T; 0 U; 0 Other;

Query Match 74.0%; Score 299.6; DB 10; Length 483;
Best Local Similarity 84.1%; Pred. No. 1.3e-83;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 4 CAAGTCAAGATGCCCATGATTTAGATGCGTCACTTATGATTTGATCAGCTG 63
DB 82 CAAGTCAAGATGCCCATGATTTAGATGCGTCACTTATGATTTGATCAGCTG 141
QY 64 AAAAATTATGTGAATGACCTGTTCCGGAATTCCTGCGGCTCCGGAAGATGTTGAGACC 123
DB 142 AAAAATTATGTGAATGACCTGTTCCGGAATTCCTGCGGCTCCGGAAGATGTTGAGACC 201
QY 124 AACTGTGAGTGTCCGTTTCTCTGTTTCCAGAAACCCAGCTGAATCCGCAACACC 183
DB 202 AACTGTGAGTGTCCGTTTCTCTGTTTCCAGAAACCCAGCTGAATCCGCAACACC 261
QY 184 GGTACCAACGATCATCATCAAGCTTCCATTTAAAGCTGAACGTTAAACCGCGCTCC 243
DB 262 GGAATCATTAAGATTAATCATATGATTAATTAAGCTGAAGGAAACCACTTCC 321
QY 244 ACCAAGCAGAGTGTGCTGTCAGAAACACCGTCTGACCTGCGCTGTGATTTCTTATGAG 303
DB 322 ACAATGTCAGGAGAGACAGAAACACAGACTAACGCTTATGATTTCTTATGAG 381
QY 304 AAAAATCCGCGGAAAGATTCCTGGAACGTTTCAATTCCTGCTGCGAAGATGATTCAC 363
DB 382 AAAAATCCGCGGAAAGATTCCTGGAACGTTTCAATTCCTGCTGCGAAGATGATTCAC 441
QY 364 CAGCAGCTGTCTCTGTCAGAAACACCGTCTGACCTGCGCTGTGATTTCTTATGAG 405
DB 442 CAGCAGCTGTCTCTGTCAGAAACACCGGAAAGTGAAGATTCCTGA 483

RESULT 5
ADP19792
ID ADP19792 standard; DNA; 483 BP.

XX AC ADP19792;

XX DT 26-AUG-2004 (first entry)

XX DE Human zalphall ligand fragment seqid 63.

XX KW cytoskeletal; zalphall ligand; pharmaceutical; cancer; immune response;
XX KM melanoma; tumour; solid tumour; haematopoietic tumour; lymphoma; human;
XX de.

XX OS Homo sapiens.

XX PN US2004110932-A1.

XX PD 10-JUN-2004.

XX PF 10-SEP-2003; 2003US-00659684.

XX PR 09-MAR-1999; 99US-0123547P.

XX PR 11-MAR-1999; 99US-0123904P.

XX PR 01-JUL-1999; 99US-0142013P.

XX PR 09-MAR-2000; 2000US-00522217.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD,
XX PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK,

DR WPI; 2004-440401/41.

XX PT New zalphall ligand polynucleotide and polypeptide molecules, useful for
XX PT treating cancer, e.g. melanoma, solid tumor, hematopoietic tumor, or
XX PT lymphoma.

XX PS Example 25; SEQ ID NO 63; 111bp; English.

CC The invention describes an isolated polypeptide comprising a sequence of
CC amino acid residues that is at least 90 or 95% identical to residues 41
CC (Gln) to 148 (Ile), or 32 (Gln) to 148 (Ile) of a sequence of 162 amino
CC acids (SEQ ID NO:2, human zalphall ligand), fully defined in the
CC specification. Also described are: a pharmaceutical composition
CC comprising the polypeptide, and a vehicle; a method of treating cancer in
CC a mammal; a method of stimulating an immune response in a mammal with
CC melanoma; a method of stimulating an immune response in a mammal bearing
CC a tumour; an isolated polynucleotide comprising a sequence of nucleotides
CC that encode amino acid residues cited above, where the polynucleotide
CC encodes a polypeptide that binds a receptor comprising 538 amino acids,
CC fully defined in the specification; a pharmaceutical composition
CC comprising the polynucleotide encoding, in a pharmaceutically acceptable
CC vehicle, an expression vector comprising the following operably linked
CC elements: a control element; and a DNA segment comprising the
CC polynucleotide; and an isolated polynucleotide molecule comprising at
CC least 10 nucleotides of the polynucleotide sequence of 642 bp, fully
CC defined in the specification. The molecules, compositions and methods are
CC useful for treating cancer, e.g. melanoma, solid tumour, hematopoietic
CC tumour, or lymphoma. This sequence represents a human zalphall ligand
CC polynucleotide used in the creation of a zalphall ligand expression
XX vector.

SQ Sequence 483 BP; 167 A; 103 C; 96 G; 117 T; 0 U; 0 Other;

Query Match 74.0%; Score 299.6; DB 12; Length 483;
Best Local Similarity 84.1%; Pred. No. 1.3e-83;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 4 CAAGTCAAGATGCCCATGATTTAGATGCGTCACTTATGATTTGATCAGCTG 63
DB 82 CAAGTCAAGATGCCCATGATTTAGATGCGTCACTTATGATTTGATCAGCTG 141
QY 64 AAAAATTATGTGAATGACCTGTTCCGGAATTCCTGCGGCTCCGGAAGATGTTGAGACC 123
DB 142 AAAAATTATGTGAATGACCTGTTCCGGAATTCCTGCGGCTCCGGAAGATGTTGAGACC 201
QY 124 AACTGTGAGTGTCCGTTTCTCTGTTTCCAGAAACCCAGCTGAATCCGCAACACC 183
DB 202 AACTGTGAGTGTCCGTTTCTCTGTTTCCAGAAACCCAGCTGAATCCGCAACACC 261
QY 184 GGTACCAACGATCATCATCAAGCTTCCATTTAAAGCTGAACGTTAAACCGCGCTCC 243
DB 262 GGAATCATTAAGATTAATCATATGATTAATTAAGCTGAAGGAAACCACTTCC 321
QY 244 ACCAAGCAGAGTGTGCTGTCAGAAACACCGTCTGACCTGCGCTGTGATTTCTTATGAG 303
DB 322 ACAATGTCAGGAGAGACAGAAACACAGACTAACGCTTATGATTTCTTATGAG 381
QY 304 AAAAATCCGCGGAAAGATTCCTGGAACGTTTCAATTCCTGCTGCGAAGATGATTCAC 363
DB 382 AAAAATCCGCGGAAAGATTCCTGGAACGTTTCAATTCCTGCTGCGAAGATGATTCAC 441
QY 364 CAGCAGCTGTCTCTGTCAGAAACACCGTCTGACCTGCGCTGTGATTTCTTATGAG 405
DB 442 CAGCAGCTGTCTCTGTCAGAAACACCGGAAAGTGAAGATTCCTGA 483

RESULT 6
ADV96416
ID ADV96416 standard; cDNA; 483 BP.

XX AC ADV96416;

XX DT 10-MAR-2005 (first entry)


```
XX DE Human zalphall ligand cDNA sequence - SEQ ID 63.
XX KW stem cell; cell culture; zalphall ligand; ss.
XX OS Homo sapiens.
XX PN US2004260065-A1.
XX
XX PD 23-DEC-2004.
XX PF 26-FEB-2004; 2004US-00787442.
XX PR 09-MAR-1999; 98US-0123547P.
XX PR 11-MAR-1999; 98US-0123904P.
XX PR 01-JUL-1999; 99US-0142013P.
XX PR 09-MAR-2000; 2000US-00522217.
XX
XX PA (NOVA/) NOVAK J E.
XX PA (PRES/) PRESNELL S R.
XX PA (SPRE/) SPRECHER C A.
XX PA (FOST/) FOSTER D C.
XX PA (HOLL/) HOLLY R D.
XX PA (GROS/) GROSS J A.
XX PA (JOHN/) JOHNSTON J V.
XX PA (NELS/) NELSON A J.
XX PA (DILL/) DILLON S R.
XX PA (HAMM/) HAMMOND A K.
XX
XX PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
XX PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX
XX DR WPI; 2005-030783/04.
XX
XX PT New zalpha 11 ligand fusion protein, useful for stimulating the
XX PT proliferation and/or development of hematopoietic cells in vitro and in
XX PT vivo, and in autologous marrow culture.
XX
XX PS Example 25; SEQ ID NO 63; 110pp; English.
XX
XX CC The invention comprises a fusion protein that contains a zalphall ligand
XX CC and a cytokine polypeptide (e.g. IL-2, IL-4, IL-15 or GM-CSF), the fusion
XX CC protein of the invention binds to the human receptor protein. The protein
XX CC of the invention is useful for stimulating the proliferation and/or
XX CC development of hematopoietic cells. The protein of the invention is also
XX CC useful in autologous marrow culture. The present cDNA sequence represents
XX CC a fragment of the human zalphall ligand coding sequence.
XX
XX SQ Sequence 483 BP, 167 A, 103 C, 96 G, 117 T, 0 U; 0 Other;
XX
XX Query Match 74.0%; Score 299.6; DB 14; Length 483;
XX Best Local Similarity 84.1%; Pred. No. 1.3e-83;
XX Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
XX
XX QY 4 CAAGGTCAAGATCGCCACATGATTGAATGCGTCACTTATGATATTTGATCACTG 63
XX DB 82 CAAGGTCAAGATCGCCACATGATTGAATGCGTCACTTATGATATTTGATCACTG 141
XX QY 64 AAAAAATTATGTGAATGACCTGTTCCGGAATTCGCGCGTCCGGAAGATGTTAGACC 123
XX DB 142 AAAAAATTATGTGAATGACCTGTTCCGGAATTCGCGCGTCCGGAAGATGTTAGACA 201
XX
XX QY 124 AACTGTGAGTGGTCCGCTTTCTCTGTTTCCAGAAAGCCAGCTGAATCCGCAACAC 183
XX DB 202 AACTGTGAGTGGTCCGCTTTCTCTGTTTCCAGAAAGCCAGCTGAATCCGCAACAC 261
XX QY 184 GGTAAACAAGACGATATCAATGATTAATAAAGTGAAGAGTAAACCGCGCTCC 243
XX DB 262 GGAACCAATGAAGATATCAATGATTAATAAAGTGAAGAGTAAACCACTTCC 321
XX QY 244 ACCAAGCAGAGTCCGTCGACGAACAACGTCGACCTGCGCTCTGTGATCTTATAG 303
XX DB 322 ACAATGACGAGGAGGAACAGAAACACAGACTTAACATGCTCTTCAATGATCTTATAG 381
```

```
QY 304 AAAAAACCGCGGAAGATTCCTGGAACGTTTCAAAATCCCTGTCGAGAAATGATTCAC 363
DB 382 AAAAAACCAACCAAGAAATTCCTTGAAGAAATGATTAATCACTTCCAAAGATGATCAT 441
QY 364 CAGCACCTGTCTCTCTGATCCACGCTTCCGAAGATTCCTGA 405
DB 442 CAGCATCTGTCTCTCTGATCAACACGGAAGTGAAGATTCCTGA 483
XX
XX RESULT 7
XX ADM41016
XX ID ADM41016 standard; DNA; 488 BP.
XX AC ADM41016;
XX DT 15-JUL-2004 (first entry)
XX DE Human IL-21 encoding DNA, seq id 1.
XX
XX KW Antiallergic; antiaesthetic; antiparasitic; antiinflammatory;
XX KW antihelminthic; dermatological; immunomodulator; interleukin; IL-21;
XX KW eosinophil; allergic; parasitic; asthma; allergic rhinitis;
XX KW helminthic infection; gene; ds.
XX
XX OS Homo sapiens.
XX PN WO2004032953-A1.
XX
XX PD 22-APR-2004.
XX PF 13-OCT-2003; 2003WO-DK000691.
XX PR 11-OCT-2002; 2002DK-00001546.
XX PR 16-OCT-2002; 2002DK-00001587.
XX PR 17-OCT-2002; 2002US-0419225P.
XX
XX PA (NOVO ) NOVO NORDISK AS.
XX
XX PI Romer J, Moller NPH, Skak K;
XX
XX DR WPI; 2004-340821/31.
XX
XX PT Use of Interleukin-21 for the treatment of diseases or conditions where
XX PT eosinophils are involved in a protective response in a subject, e.g.
XX PT allergic conditions and/or parasitic diseases.
XX
XX PS Disclosure; SEQ ID NO 1; 32pp; English.
XX
XX CC The invention relates to an interleukin (IL)-21 that is used for the
XX CC treatment of diseases or conditions where eosinophils are involved in a
XX CC protective response in a subject, e.g. allergic conditions and/or
XX CC parasitic diseases. Methods of the invention are useful for the treatment
XX CC of diseases or conditions where eosinophils are involved in a protective
XX CC response in a subject, such as allergic conditions (e.g. asthma, allergic
XX CC rhinitis or allergic diseases of the skin) and/or parasitic diseases,
XX CC especially helminthic infection. The current sequence represents the cDNA
XX CC sequence encoding IL-21. Note: This sequence does not decode to that of
XX CC ADM41017, which we are told in the specification is the amino acid
XX CC sequence of IL-21.
XX
XX SQ Sequence 488 BP, 170 A, 103 C, 98 G, 117 T, 0 U; 0 Other;
XX
XX Query Match 74.0%; Score 299.6; DB 12; Length 488;
XX Best Local Similarity 84.1%; Pred. No. 1.3e-83;
XX Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
XX
XX QY 4 CAAGGTCAAGATCGCCACATGATTGAATGCGTCACTTATGATATTTGATCACTG 63
XX DB 87 CAAGGTCAAGATCGCCACATGATTGAATGCGTCACTTATGATATTTGATCACTG 146
XX QY 64 AAAAAATTATGTGAATGACCTGTTCCGGAATTCGCGCGTCCGGAAGATGTTAGACC 123
```

```

Db 147 AAAAAATTATGTGAATGACTGTCCTGTAATTTCTGCAGCTCCAGAAATGTAGAGCA 206
Qy 124 AACTGTAGTGTGTCCTGTTCTCTGTTTCCAGAAAGCCGCTGAAATCCGCAAAACC 183
Db 207 AACTGTAGTGTGTCCTGTTTCTGTTTCCAGAAAGCCGCTGAAATCCGCAAAATACA 266
Qy 184 GGTACACAGCAACGTATCATCAAGTTTCCATTAATAAACTGAAGCTAAACCGCCGTC 243
Db 267 GGAACCAATGAAGATATCAATGATCAATTAATAAAAGCTGAAGAGAAACCACTTCC 326
Qy 244 ACCAAGCAGTGTCTGTCTGAGAAACACCGTCTGACCTGCTGTGATTTATGAG 303
Db 327 ACAATGTGAGGAGAAACAGAAACACAGACTAATGACCTGATGATTTATGAG 386
Qy 304 AAAAAACCGCGGAAGAAATTCCTGGAAGCTTCAATCCCTGCTGCAAGAAATGATTCAC 363
Db 387 AAAAAACCAACCAAGAAATTCCTGGAAGAAATTCCTGCAAGAAATGATTCAT 446
Qy 364 CAGCAGCTGTCTGTCTGTACCCAGCTTCCGAAATTCCTGA 405
Db 447 CAGCATCTGTCTTCTTGAACACAGGAAATGAAATTCCTGA 488

RESULT 8
ID ADF17040 standard; DNA; 489 BP.
AC ADF17040;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human albumin fusion protein-related DNA sequence SegID2157.
XX
KW albumin fusion protein; albumin activity; human serum albumin;
KM serum osmotic pressure; shelf-life; stability; antidiabetic;
XX gene therapy; diabetes mellitus; human; gene; ds.
OS Homo sapiens.
XX
PN WO2003060071-A2.
XX
PD 24-JUL-2003.
XX
PE 23-DEC-2002; 2002MO-US040891.
XX
XX 21-DEC-2001; 2001US-0341811P.
PR 24-JAN-2002; 2002US-0350358P.
PR 28-JAN-2002; 2002US-0351360P.
PR 26-FEB-2002; 2002US-0359370P.
PR 28-FEB-2002; 2002US-0360000P.
PR 27-MAR-2002; 2002US-0367500P.
PR 08-APR-2002; 2002US-0370227P.
PR 10-MAY-2002; 2002US-0378950P.
PR 24-MAY-2002; 2002US-0382617P.
PR 28-MAY-2002; 2002US-0383123P.
PR 05-JUN-2002; 2002US-0385708P.
PR 10-JUL-2002; 2002US-0394625P.
PR 24-JUL-2002; 2002US-0398008P.
PR 09-AUG-2002; 2002US-0402131P.
PR 13-AUG-2002; 2002US-0402708P.
PR 18-SEP-2002; 2002US-0411355P.
PR 18-SEP-2002; 2002US-0411426P.
PR 02-OCT-2002; 2002US-0414984P.
PR 11-OCT-2002; 2002US-0417611P.
PR 23-OCT-2002; 2002US-0420246P.
PR 05-NOV-2002; 2002US-0423623P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (DBLZ-) DELTA BIOTECHNOLOGY LTD.
PA (PRIN-) PRINCIPIA PHARM CORP.
PI Balance DJ, Turner AJ, Rosen CA, Haseltine WA,
XX

```

```

DR WPI; 2003-598517/56.
DR P-RSD; ADF17046.
XX
PT New albumin fusion protein, useful for preparing a composition for
PT treating diabetes mellitus.
XX
PS Example 4; SEQ ID NO 2157; 24dp; English.
XX
CC This invention relates to a novel albumin fusion protein having albumin
CC or biological activity. Human serum albumin is responsible for a
CC significant proportion of the osmotic pressure of serum and also
CC functions as a carrier of endogenous and exogenous ligands. The fusion of
CC albumin to a therapeutic protein may increase shelf-life and stability of
CC the therapeutic protein. The albumin fusion protein of the invention may
CC allow production of compositions with antidiabetic activity whilst the
CC nucleotide sequence which encodes it may be useful for gene therapy. The
CC albumin fusion protein is useful for preparing a composition for treating
CC diabetes mellitus. The present sequence is a DNA sequence which encodes a
CC therapeutic protein which was fused with human albumin to create a novel
CC albumin fusion protein of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/publishedpct_sequences
XX
SQ Sequence 489 BP; 170 A; 103 C; 98 G; 118 T; 0 U; 0 Other;
XX
Query Match 74.0%; Score 299.6; DB 10; Length 489;
Best Local Similarity 84.1%; Pred. No. 1,3e-83;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
XX
Qy 4 CAAGTCAAGATGCCCATGATTAAGATGCTCACTTATATATTTGATCAGCTG 63
Db 88 CAGGTCAAGATGCCCATGATTAAGATGCTCACTTATATATTTGATCAGCTG 147
Qy 64 AAAAAATTATGTGAATGACTGTCCTGGAATTCCTGCGGCTCCGAAAGTTGAGACC 123
Db 148 AAAAAATTATGTGAATGACTGTCCTGGAATTCCTGCGGCTCCGAAAGTTGAGACA 207
Qy 124 AACTGTAGTGTGTCCTGTTCTCTGTTTCCAGAAAGCCAGCTGAAATCCGCAAAACC 183
Db 208 AACTGTAGTGTGTCCTGTTTCTCTGTTTCCAGAAAGCCAGCTGAAATCCGCAAAATACA 267
Qy 184 GGTACACAGCAACGTATCATCAAGTTTCCATTAATAAACTGAAGCTAAACCGCCGTC 243
Db 268 GGAACCAATGAAGATATCAATGATCAATTAATAAAAGCTGAAGAGAAACCACTTCC 327
Qy 244 ACCAAGCAGTGTCTGTCTGAGAAACACCGTCTGACCTGCTGTGATTTATGAG 303
Db 328 ACAATGTGAGGAGAAACAGAAACACAGACTAATGACCTGATGATTTATGAG 387
Qy 304 AAAAAACCGCGGAAGAAATTCCTGGAAGCTTCAATCCCTGCTGCAAGAAATGATTCAC 363
Db 388 AAAAAACCAACCAAGAAATTCCTGGAAGAAATTCCTGCAAGAAATGATTCAT 447
Qy 364 CAGCAGCTGTCTGTCTGTACCCAGCTTCCGAAATTCCTGA 405
Db 448 CAGCATCTGTCTTCTTGAACACAGGAAATGAAATTCCTGA 489

RESULT 9
ID ADV42801 standard; cDNA; 489 BP.
AC ADV42801;
XX
DT 10-MAR-2005 (first entry)
XX
DE Human psychoneuroendocrine-immune expressed sequence tag SEQ ID NO 429.
XX
KW microarray; psychoneuroendocrine-immune; chronic fatigue;
KM non-insulin dependent diabetes; allergy; immune disorder; inflammation;
KW cancer; neoplasm; infection; expressed sequence tag; ss.
XX

```

OS Homo sapiens.
 XX PN WO2004108899-A2.
 XX PD 16-DEC-2004.
 XX PF 04-JUN-2004; 2004WO-US017686.
 XX PR 04-JUN-2003; 2003US-0475915P.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Nicholson A, Vernon SD;
 XX DR WPI; 2005-031682/03.
 XX PT New microarray comprising probes for genes involved in
 PT psychoneuroendocrine immune (PNI) activity, useful in diagnosing a
 PT condition associated with PNI activity, e.g., inflammatory or infectious
 PT diseases.
 XX PS Claim 1; SEQ ID NO 429; 254bp; English.
 XX CC The invention relates to a new microarray which comprises probes for
 CC genes involved in psychoneuroendocrine immune (PNI) activity. The
 CC microarray is useful in diagnosing a condition associated with PNI
 CC activity, such as CFS, type-2 diabetes, allergic condition, inflammation,
 CC cancer and infection. The present sequence represents a
 CC psychoneuroendocrine immune gene expressed sequence tag. Note the
 CC specification mentions SEQ ID NO of up to 3314 but only sequences up to
 CC SEQ ID NO 1829 are provided.
 XX SQ Sequence 489 BP; 170 A; 103 C; 98 G; 118 T; 0 U; 0 Other;

Query Match 74.0%; Score 299.6; DB 14; Length 489;
 Best Local Similarity 84.1%; Pred. No. 1.3e-83;
 Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 4 CAAGGTCAAGATCCGACATGATTGAATGCGTCACTTATGATTTGTTGATCAGCTG 63
 DB 88 CAAGGTCAAGATCCGACATGATTGAATGCGTCACTTATGATTTGTTGATCAGCTG 147
 QY 64 AAAAATTATGTAATGATGACTGCTTCCGGAATTCGCGCGGCTCCGGAAGATGTTGAGACC 123
 DB 148 AAAAATTATGTAATGATGACTGCTTCCGGAATTCGCGCGGCTCCGGAAGATGTTGAGACC 207
 QY 124 AACTGTGAGTGGTCCGCTTTCTCTGTTCCAGAAAGCCAGCTGAATCCGCAAAACACC 183
 DB 208 AACTGTGAGTGGTCCGCTTTCTCTGTTCCAGAAAGCCAGCTGAATCCGCAAAACACC 267
 QY 184 GGTAAACAAGACGTATCATCACTTTCAATTAAAAAAGTGAACGTAAACCGCGCTCC 243
 DB 268 GGAACAATGAAGATATCATATGATTAATTAAGGTGAAGAGAAACACACTTCC 327
 QY 244 ACCAAGCGAGTGGTCCGCTTCAAAAACACCGCTGACCTCCGCTCTGATTTCTTATAG 303
 DB 328 ACAATATGAGGAGAGAGACAGAAACAGACTTAACATCCCTTCAATGATTTCTTATAG 387
 QY 304 AAAAAGCCGCGAAGAAATTCCTGGAAGTTTCAAAATCCGCTGACAGAAATGATTCAC 363
 DB 388 AAAAAGCCGCGAAGAAATTCCTGGAAGTTTCAAAATCCGCTGACAGAAATGATTCAT 447
 QY 364 CAGACCTGTCTCTCTGTTACCAACGTTCCGAAGATTCCTGA 405
 DB 448 CAGCATGTCTCTCTGTTACCAACGTTCCGAAGATTCCTGA 489

RESULT 10
 AAA75552
 ID AAA75552 standard; DNA; 642 BP.
 XX AC AAA75552;
 XX

DT 22-JAN-2001 (first entry)
 XX DE DNA encoding a human zalphall ligand polypeptide.
 XX KW zalphall ligand; cytokine; haematopoietic cell proliferation; lymphoma;
 XX KM tumorigenesis; leukaemia; hematopoiesis; B cell tumour; ss.
 XX OS Homo sapiens.
 XX FH Key
 XX FT CDS
 XX FT Location/Qualifiers
 XX FT 47..535
 XX FT /tag= a
 XX FT /product= "Zalphall"
 XX PN WO200053761-A2.
 XX PD 14-SEP-2000.
 XX PF 09-MAR-2000; 2000WO-US006067.
 XX PR 09-MAR-1999; 99US-00264908.
 XX PR 11-MAR-1999; 99US-00265992.
 XX PR 01-JUL-1999; 99US-0142013P.
 XX PA (ZYMO) ZYMOGENETICS INC.
 XX PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
 XX PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
 XX DR WPI; 2000-565600/52.
 XX DR P-PSDB; AAB18623.

PT New human cytokine, designated zalphall ligand, useful for stimulating
 PT the proliferation and/or development of hematopoietic cells in vitro and
 PT in vivo, and for treating tumorigenesis.
 PS Claim 14; Page 204-205; 256bp; English.

XX CC The present sequence encodes a human zalphall ligand polypeptide, which
 CC is a cytokine. The zalphall ligand is useful for stimulating the
 CC proliferation and development of haematopoietic cells in vitro and in
 CC vivo. Zalphall ligand polynucleotides can be used as primers or probes
 CC for cloning the zalphall gene. The zalphall ligand is useful for treating
 CC tumorigenesis. A zalphall ligand-sepoxin fusion toxin may be used for
 CC treating leukaemia and lymphomas. Antagonists against zalphall ligand
 CC interaction. Antagonists are also useful for inhibiting expansion,
 CC proliferation, activation and differentiation of cells involved in
 CC regulating hematopoiesis. The zalphall ligand may also be used to
 CC stimulate an immune response against B cell tumour, a virus, a parasite
 CC or a bacterium. The zalphall polypeptides, polynucleotides, antagonists,
 CC agonists and antibodies are also useful for the detection, diagnosis,
 CC prevention, and treatment of diseases associated with a zalphall ligand
 CC genetic defect

XX SQ Sequence 642 BP; 220 A; 127 C; 129 G; 166 T; 0 U; 0 Other;

Query Match 74.0%; Score 299.6; DB 3; Length 642;
 Best Local Similarity 84.1%; Pred. No. 1.5e-83;
 Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 4 CAAGGTCAAGATCCGACATGATTGAATGCGTCACTTATGATTTGTTGATCAGCTG 63
 DB 134 CAAGGTCAAGATCCGACATGATTGAATGCGTCACTTATGATTTGTTGATCAGCTG 193
 QY 64 AAAAATTATGTAATGATGACTGCTTCCGGAATTCGCGCGGCTCCGGAAGATGTTGAGACC 123
 DB 194 AAAAATTATGTAATGATGACTGCTTCCGGAATTCGCGCGGCTCCGGAAGATGTTGAGACC 253
 QY 124 AACTGTGAGTGGTCCGCTTTCTCTGTTCCAGAAAGCCAGCTGAATCCGCAAAACACC 183
 DB 254 AACTGTGAGTGGTCCGCTTTCTCTGTTCCAGAAAGCCAGCTGAATCCGCAAAATCA 313

```
QY 184 GGTAAACAGCAGATCATCAACGTTTCATTAAAGAAAGCTAAACCGCGCTCC 243
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 314 GGAAACATGAAGATGAATCATATGATCAATTAAGAGTAAAGAGAAACCACTTCC 373
QY 244 ACCAAGCAGATGCTGCTGAGAAACACCGTCTGACTGCGCGTCTGTATTTATGAG 303
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 374 ACAAGTCAAGGAGAGACAGAAACACAGACTAACATGCCCTTCATGTATTTATGAG 433
QY 304 AAAAACCAGGAGAAAGATTCCTGGAACGTTTCAAAATCCCTGCTGCAGAAATGATTCAC 363
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 434 AAAAACCAGGAGAAAGATTCCTGGAAGATTCCTGGAAGATTCCTGGAAGATTCAT 493
QY 364 CAGCAGCTGCTCTCTGCTACCAAGCTTCGGAAGATTCCTGA 405
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 494 CAGCATCTGCTCTTGAACACACGGAAGTGAAGATTCCTGA 535

RESULT 11
AAS20637
ID AAS20637 standard; cDNA; 642 BP.
XX
AC AAS20637;
XX
DT 09-APR-2002 (first entry)
XX
DE cDNA encoding human zalphall1 ligand polypeptide.
XX
KW Cytokine; zalphall1 ligand; zalphall1 receptor; NK cell progenitor;
KW natural killer cell proliferation; T-cell proliferation;
KW B-cell proliferation; anti-tumour response; immune system;
KW immunostimulant; cytoelastic; human; gene therapy; hPBGS;
KW activated human peripheral blood cell; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 47..535
FT /tag= a
FT /product= "Zalphall1 ligand"
FT sig_peptide 47..139
FT /tag= b
FT mat_peptide 140..532
FT /tag= c
XX
PN US6307024-B1.
XX
PD 23-OCT-2001.
XX
PF 09-MAR-2000; 2000US-00522217.
XX
PR 09-MAR-1999; 99US-0123547P.
PR 11-MAR-1999; 99US-0123904P.
PR 01-JUL-1999; 99US-0142013P.
XX
PA (Zymo ) ZYMOGENETICS INC.
XX
PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD,
PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX
DR P-PSDB; AAU11965.
XX
XX WPI; 2002-040208/05.
XX
PT New zalphall1 ligand polypeptides and polynucleotides, useful for
PT stimulating proliferation, activation, differentiation and/or induction
PT of inhibition of specialized cell function, or for stimulating an
PT antigenic response.
XX
XX Example 7; Col 123-126; 105pp; English.
XX
XX The present invention relates to the isolation of a novel cytokine,
XX zalphall1 ligand and the polynucleotide encoding it. The invention also
XX gives the sequence for the zalphall1 receptor and the polynucleotide
XX encoding it. The zalphall1 ligand polypeptide stimulates proliferation of
```

```
CC natural killer (NK) cells or NK cell progenitors, the activation of NK
CC cells, proliferation of T-cells, proliferation of B-cells stimulated with
CC anti-CD40 antibodies, stimulates an antigenic response in a mammal, and
CC reduces proliferation of B-cells stimulated with anti-19M antibodies. The
CC zalphall1 ligand polypeptide is also useful in preparing antibodies that
CC bind to zalphall1 ligand epitopes. The zalphall1 ligand polynucleotides can
CC be used as probes or primers to clone regions of a zalphall1 ligand gene,
CC and in gene therapy. Zalphall1 ligand may also be used to identify
CC inhibitors of its activity, to enhance the generation of anti-tumour
CC responses with or without the infusion of donor lymphocytes, and to
CC activate or stimulate the immune system. The present sequence encoding
CC for human zalphall1 ligand polypeptide is isolated from a cDNA library
CC from activated human peripheral blood cells (hPBGS)
XX
SQ Sequence 642 BP; 220 A; 127 C; 129 G; 166 T; 0 U; 0 Other;
Query Match 74.0%; Score 299.6; DB 6; Length 642;
Best Local Similarity 84.1%; Pred. No. 1.5e-83;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
QY 4 CAAGTCAAGATGCCCAATGATTAAGATGCTCAACTTATGATTTGTTGATCACTG 63
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 134 CAAGTCAAGATGCCCAATGATTAAGATGCTCAACTTATGATTTGTTGATCACTG 193
QY 64 AAAAATTATGTGATGATGACTGTTCGGAATTCCTGCGGCTCGGAAGATGTGAGACC 123
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 194 AAAAATTATGTGATGATGACTGTTCGGAATTCCTGCGGCTCGGAAGATGTGAGACC 253
QY 124 AACTGTGATGTGCTGCTGCTTCTCTGTTTCCAGAAAGCCAGCTGAAATCCGAAACACC 183
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 254 AACTGTGATGTGCTGCTGCTTCTCTGTTTCCAGAAAGCCAGCTGAAATCCGAAACACC 313
QY 184 GGTAAACAGCAGATCATCAACGTTTCATTAAAGAAAGCTAAACCGCGCTCC 243
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 314 GGAAACATGAAGATGAATCATATGATCAATTAAGAGTAAAGAGAAACCACTTCC 373
QY 244 ACCAAGCAGATGCTGCTGAGAAACACCGTCTGACTGCGCGTCTGTATTTATGAG 303
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 374 ACAAGTCAAGGAGAGACAGAAACACAGACTAACATGCCCTTCATGTATTTATGAG 433
QY 304 AAAAACCAGGAGAAAGATTCCTGGAACGTTTCAAAATCCCTGCTGCAGAAATGATTCAC 363
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 434 AAAAACCAGGAGAAAGATTCCTGGAAGATTCCTGGAAGATTCCTGGAAGATTCAT 493
QY 364 CAGCAGCTGCTCTCTGCTACCAAGCTTCGGAAGATTCCTGA 405
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 494 CAGCATCTGCTCTTGAACACACGGAAGTGAAGATTCCTGA 535

RESULT 12
AAD47852
ID AAD47852 standard; DNA; 642 BP.
XX
AC AAD47852;
XX
DT 27-AUG-2003 (first entry)
XX
DE Human interleukin-21 (IL-21) DNA.
XX
XX Interleukin-21; IL-21; antagonist; cancer; inflammatory;
XX autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
KW systemic lupus erythematosus; myasthenia gravis; diabetes; human;
KW zalphall1 ligand; de.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 47..535
FT /tag= a
FT /product= "IL-21"
XX
XX WO2003040313-A2.
```

PD 15-MAY-2003.
XX 28-OCT-2002; 2002WO-US034502.
XX 05-NOV-2001; 2001US-0337586P.
XX (ZYMO) ZYMOGENETICS INC.
XX Presnell SR, West JW, Novak JE;
XX WPI; 2003-441547/41.
XX P-PSDB; AAE14932.
XX
XX New IL-21 polypeptide and encoding polynucleotide, useful for diagnosing
XX PT and treating disorders with aberrant expression or activity of the IL-21
XX PT polypeptide, such as cancer, rheumatoid arthritis, multiple sclerosis and
XX PT diabetes.
XX
XX Disclosure; Page 52-53; 71pp; English.
XX
XX The invention relates to polynucleotides and polypeptides of interleukin-
XX CC 21 (IL-21) antagonists, that bind with specificity and exhibit an EC50
XX CC that is not detectable in receptor binding studies. The antagonists of
XX CC the invention have mutations in the D helix of the IL-21 molecule, and
XX CC can be used to inhibit the activity of IL-21 with its cognate receptor.
XX CC The IL-21 antagonists are useful for diagnosing and treating disorders
XX CC involving the aberrant expression or activity of the IL-21 polypeptide,
XX CC such as cancer, inflammatory and autoimmune disorders, including
XX CC rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus,
XX CC myasthenia gravis and diabetes. The polypeptides can also be used to
XX CC prepare antibodies that bind IL-21 epitopes, peptides or polypeptides,
XX CC and for enhancing in vivo killing of target tissues. The present sequence
XX CC is human IL-21 (originally designated zalphal1 ligand) DNA
XX
SQ Sequence 642 BP; 220 A; 127 C; 129 G; 166 T; 0 U; 0 Other;

Query Match 74.0%; Score 299.6; DB 9; Length 642;
Best Local Similarity 84.1%; Pred. No. 1.5e-83;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 4 CAAGTCAAGATCGGCACATGATTTAGATGCGTCACTTATGATTTGATCAGCTG 63
DB 134 CAAGTCAAGATCGGCACATGATTTAGATGCGTCACTTATGATTTGATCAGCTG 193
QY 64 AAAAATTATGTAATGATGATGCTGCTCGGATTCCTGCGGCTCCGGAAGATTGAGACC 123
DB 194 AAAAATTATGTAATGATGATGCTGCTCGGATTCCTGCGGCTCCGGAAGATTGAGACC 253
QY 124 AACTGTGATGCTCGCTTTCTCTGTTTCCAGAAAGCCGAGCTGAATTCGCAAAACACC 183
DB 254 AACTGTGATGCTCGCTTTCTCTGTTTCCAGAAAGCCGAGCTGAATTCGCAAAACACC 313
QY 184 GGTAAACAAGAACGATCATCAAGTTTCCATTTAAAAAGTAAACGTAACCGCGCGCC 243
DB 314 GGAACAATGAAGATTAATTAATGATTAATTAAGAGGAGGAGAAACCACTTCC 373
QY 244 ACCAAGCAGAGTCTGCTGACAGAAACCCGCTGACCTGCTGATTTCTTATGAG 303
DB 374 ACAATGAGAGGAGAGACAGAAACAGACATCAATCCCTTATGATTTCTTATGAG 433
QY 304 AAAAAACCGCCGAAAGAAATTTCTGGAACGTTTCAATCCCTGCTGACAGAAATGATTCAC 363
DB 434 AAAAAACCGCCGAAAGAAATTTCTGGAACGTTTCAATCCCTGCTGACAGAAATGATTCAT 493
QY 364 CAGCAGCTGCTCTGCTGACAGAGGTTCCGAAAGTTCTCTGA 405
DB 494 CAGCAGCTGCTCTGCTGACAGAGGTTCCGAAAGTTCTCTGA 535

RESULT 13
ADH44571
XX ADH44571 standard; cDNA; 642 BP.
XX

AC ADH44571;
XX 25-MAR-2004 (first entry)
XX
XX Human CDNA encoding Zalphal1 ligand.
XX
XX Human; ss; Zalphal1 ligand; Zalphal1 receptor; immune response;
XX KW tumour progression; metastasis; tumour stasis; haematopoietic tumour;
XX KW lymphoma; B cell tumour; systemic lupus erythematosus;
XX KW rheumatoid arthritis; myasthenia gravis; diabetes; infectious disease;
XX KW immunocompromised patient; HIV infection; vaccine; chromosome 4q27.
XX
XX Homo sapiens.
XX
XX US6605272-B2.
XX
XX 12-AUG-2003.
XX
XX 03-AUG-2001; 2001US-00923246.
XX
XX 09-MAR-1999; 99US-0123547P.
XX PR 11-MAR-1999; 99US-0123904P.
XX PR 01-JUL-1999; 99US-0142013P.
XX PR 09-MAR-2000; 2000US-00522217.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
XX PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX WPI; 2003-695283/82.
XX
XX Stimulating an immune response in a mammal exposed to an antigen or
XX PT pathogen, useful for enhancing anti-tumor activity resulting in reduced
XX PT tumor progression or metastasis, comprises administering zalphal1 ligand
XX PT polypeptide.
XX
XX Example 7; SEQ ID NO 1; 103pp; English.
XX
XX The invention relates to stimulating an immune response in a mammal
XX CC exposed to an antigen or pathogen comprising administering a composition
XX CC comprising mature zalphal1 ligand polypeptide comprising residues 32-162
XX CC of ADH44572 in a pharmaceutical vehicle. Also included are stimulating an
XX CC immune response in a mammal exposed to an antigen or pathogen
XX CC (comprising: (a) determining (indirectly) the level of antigen or
XX CC pathogen present in the mammal; (b) administering a composition
XX CC comprising zalphal1 ligand polypeptide in a pharmaceutical vehicle; (c)
XX CC determining (indirectly) the level of antigen or pathogen in the mammal;
XX CC and (d) comparing the antigen or pathogen level in (a) with (b), where a
XX CC change in the level indicates stimulation of immune response), and
XX CC stimulating an immune response in a mammal exposed to an antigen or
XX CC pathogen (comprising: (a) determining a level of antigen- or pathogen-
XX CC specific antibody; (b) administering a composition comprising zalphal1
XX CC ligand polypeptide in a pharmaceutical vehicle; (c) determining a post
XX CC administration level of the antigen- or pathogen-specific antibody; and
XX CC (d) comparing the level of the antibody in (a) with (b), where an
XX CC increase in the antibody level indicates stimulation of immune response).
XX CC The method is useful for stimulating an immune response in a mammal
XX CC exposed to an antigen or pathogen, and for enhancing anti-tumour activity
XX CC resulting in a reduction in tumour progression, decrease in metastasis,
XX CC or tumour stasis. The tumour may be a haematopoietic tumour, a lymphoma
XX CC or a B cell tumour. The zalphal1 ligand is useful for treating a wide
XX CC range of diseases arising from defects in the immune system, e.g.
XX CC systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis, or
XX CC diabetes, for boosting immunity to infectious diseases, treating
XX CC immunocompromised patients, such as HIV+ patients and in improving
XX CC vaccines. The present sequence is a human zalphal1 ligand cDNA (or
XX CC fragment).
XX
SQ Sequence 642 BP; 220 A; 127 C; 129 G; 166 T; 0 U; 0 Other;

Query Match 74.0%; Score 299.6; DB 10; Length 642;
Best Local Similarity 84.1%; Pred. No. 1.5e-83;
XX

PT administering to the subject a polypeptide having a functional activity
of interleukin-21.

PS Disclosure; SEQ ID NO 1; 154pp; English.

XX
CC The invention relates to treating Non-Hodgkin's lymphoma, cancer or
CC infection and involves administering to the subject a polypeptide having
CC a functional activity of interleukin-21 (IL-21). The methods are useful
CC for treating Non-Hodgkin's lymphoma; cancer such as renal cell carcinoma,
CC epithelial carcinoma, breast cancer, prostate cancer, ovarian cancer and
CC colon cancer; viral infection such as AIDS, Hepatitis B or C virus,
CC gastroenteritis, haemorrhagic diseases, enteritis, carditis,
CC encephalitis, paralysis, brochiolitis, upper or lower respiratory
CC disease, respiratory papillomatosis, arthritis, disseminated disease,
CC meningitis, and mononucleosis; or bacterial infection, such as an
CC infection by a bacteria selected from chlamydiae, listeriae, helicobacter
CC pylori, mycobacterium, mycoplasma, salmonella, and shigella, or sudden
CC acute respiratory syndrome caused by a coronavirus, Herpes Simplex
CC viruses, Epstein-Barr virus, Cytomegalovirus, pox viruses, Papilloma
CC virus, Adenovirus, Poliovirus, Orthomyxoviruses, Paramyxoviruses,
CC Influenza viruses, caliciviruses, rabies viruses, and rinderpest viruses.
CC The present sequence represents a DNA encoding a human IL-21 polypeptide.
XX
SQ

Sequence 642 BP; 220 A; 127 C; 129 G; 166 T; 0 U; 0 Other;

Query Match 74.0%; Score 299.6; DB 12; Length 642;

Best Local Similarity 84.1%; Pred. No. 1.5e-83;

Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 4 CAAGGTCAAGATCGGCACATGATGAAATGCGTCAACTTATGATATGTTGATCAGCTG 63
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
134 CAAGGTCAAGATCGGCACATGATGAAATGCGTCAACTTATGATATGTTGATCAGCTG 193
QY 64 AAAAAATTATGTAATGACTGCTGCGAATTCCTGCGGCTCCGAAAGATGTGAGACC 123
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
194 AAAAAATTATGTAATGACTGCTGCGAATTCCTGCGGCTCCGAAAGATGTGAGACC 253
QY 124 AACTGTAGTGTGCTCGCTTTCTCTGTTTCCAGAAAGCCAGCTGAATCCGAAACACC 183
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
254 AACTGTAGTGTGCTCGCTTTCTCTGTTTCCAGAAAGCCAGCTGAATCCGAAACACC 313
QY 184 GGTACCAAGAACGTATCATCAAGTTTCCATTAAAACTGAACGTAAACGGCGCTCC 243
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
314 GGTACCAAGAACGTATCATCAAGTTTCCATTAAAACTGAACGTAAACGGCGCTCC 373
QY 244 ACCAAGCAGGTCTGCTCAGAAACACCGTGAACCTGCGCTGCTGATTTATGAG 303
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
374 ACCAAGCAGGTCTGCTCAGAAACACCGTGAACCTGCGCTGCTGATTTATGAG 433
QY 304 AAAAAACGCGAAAGAAATTCCTGGAACGTTTCAATCCCTGCTGCAGAAAAATGATTCAC 363
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
434 AAAAAACGCGAAAGAAATTCCTGGAACGTTTCAATCCCTGCTGCAGAAAAATGATTCAC 493
QY 364 CAGCACCTGTCTCTCTGTAACCAAGTTCCGAAAGATTCCTGA 405
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
494 CAGCACCTGTCTCTCTGTAACCAAGTTCCGAAAGATTCCTGA 535

Search completed: August 7, 2006, 13:13:21
Job time : 523 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2006, 12:06:06 / Search time 4431 Seconds
(without alignments)
511.110 Million cell updates/sec

Title: US-10-735-149-27

Perfect score: 405

Sequence: 1 atgcaaggctcaagatcgcca.....acggtccgaagattcctga 405

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 48236798 seqs, 2795965780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: gb_eest1:*
2: gb_eest3:*
3: gb_eest4:*
4: gb_eest5:*
5: gb_eest6:*
6: gb_hic:*
7: gb_eest2:*
8: gb_eest7:*
9: gb_eest8:*
10: gb_eest9:*
11: gb_g981:*
12: gb_g982:*
13: gb_g983:*
14: gb_g984:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	299.6	74.0	566	14 AY417615	AY417615 Homo sapi
2	299.6	74.0	569	5 CD559455	CD559455 AGENCOURT
3	299.6	74.0	573	5 CD559609	CD559609 AGENCOURT
4	299.6	74.0	581	5 CD559459	CD559459 AGENCOURT
5	299.6	74.0	582	5 CD559457	CD559457 AGENCOURT
6	299.6	74.0	582	5 CD559461	CD559461 AGENCOURT
7	299.6	74.0	583	5 CD559456	CD559456 AGENCOURT
8	299.6	74.0	583	5 CD559612	CD559612 AGENCOURT
9	299.6	74.0	592	5 CD559614	CD559614 AGENCOURT
10	299.6	74.0	599	5 CD559610	CD559610 AGENCOURT
11	298	73.6	600	5 CD559613	CD559613 AGENCOURT
12	296.4	73.2	581	5 CD559460	CD559460 AGENCOURT
13	294.2	72.6	489	14 AY417616	AY417616 Pan trogl
14	292.6	72.2	551	8 CR988723	CR988723 CR988723
15	293.2	69.9	608	5 CD559611	CD559611 AGENCOURT
16	292.8	62.4	749	5 CD559458	CD559458 AGENCOURT
17	195.8	48.3	567	3 BP369699	BP369699 BP369699
18	167.6	41.4	438	14 AY417617	AY417617 Mus muscu
19	113.2	28.0	421	5 CUI41332	CUI41332 CUI41332

C	20	100.8	24.9	450	4	BY580318	BY580318 BY580318
	21	84.2	20.8	756	13	DU302657	DU302657 109844808
	22	78.8	19.5	681	13	CZ424877	CZ424877 1020580 R
	23	78.8	19.5	709	13	CZ419965	CZ419965 1015668 R
	24	78.8	19.5	735	13	CZ427169	CZ427169 1022872 R
C	25	67.2	16.6	539	12	BZ937073	BZ937073 CH240_61E
	26	59.6	14.7	339	4	BY214337	BY214337 BY214337
	27	59.6	14.7	363	4	BY212756	BY212756 BY212756
	28	59.6	14.7	426	4	BY211567	BY211567 BY211567
	29	59.6	14.7	527	11	AZ248993	AZ248993 RPT-23-4
C	30	59.6	14.7	535	1	AA764063	AA764063 vwo9602.r
	31	59.6	14.7	697	4	BY750468	BY750468 BY750468
	32	59.6	14.7	2338	6	AK155984	AK155984 Mus muscu
	33	57.6	14.2	365	4	BY220565	BY220565 BY220565
C	34	57.4	14.2	812	2	B1561560	B1561560 603256252
C	35	50	12.3	584	13	C2026087	C2026087 CH240_498
C	36	46.4	11.5	880	14	CT053599	CT053599 Sus scrofa
	37	40.4	10.0	629	11	AZ435999	AZ435999 IM0223N20
	38	40.2	9.9	358	4	BY213329	BY213329 BY213329
	39	38.8	9.6	1302	12	B2572734	B2572734 m6h2_2773
C	40	37.8	9.3	647	11	BH013521	BH013521 TDGAT96TH
	41	37.6	9.3	1066	10	DV013822	DV013822 CNB82-D1
C	42	37.2	9.2	503	11	BH124149	BH124149 RPT-24-3
C	43	36	8.9	884	14	CNS00600	AL065923 Drosophila
C	44	36	8.9	1441	9	DNT37022	DNT37022 CNB90-E02
C	45	35.8	8.8	856	12	CC509666	CC509666 CH240_352

ALIGNMENTS

RESULT 1
AY417615
LOCUS
DEFINITION Homo sapiens IL21 gene, VIRUTAL TRANSCRIPT, partial sequence.
ACCESSION AY417615
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCES
AUTHORS
1 (bases 1 to 489)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Interfering nonneutral evolution from human-chimp-mouse orthologous
gene trios

JOURNAL
PUBMED
AUTHORS
2 (bases 1 to 489)
Science 302 (5652), 1960-1963 (2003)
14671302

TITLE
JOURNML
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.

COMMENT
FEATURES
source
Location/Qualifiers
1..489
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
1..489
/gene="IL21"
/locus_tag="HCM6283"

ORIGIN
gene
1..489
/gene="IL21"
/locus_tag="HCM6283"

Query Match 74.0%; Score 299.6; DB 14; Length 489;
Best Local Similarity 84.1%; Pred. No. 9, 5e-83;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 4 CAAGGTCAAGATCGCCATGATTTAGAAATCGTCACTTATAGATATTTGATCAGCTG 63
DB 88 CAAGGTCAAGATCGCCATGATTTAGAAATCGTCACTTATAGATATTTGATCAGCTG 147
QY 64 AAAAATTTATGTAATGACCTGTTCCGGAATTCCTGCGGCTCCGGAAGATGTTAGACC 123
DB 148 AAAAATTTATGTAATGACCTGTTCCGGAATTCCTGCGGCTCCGGAAGATGTTAGACC 207
QY 124 AACTGTAGTGTGCGCTTCTCTGTTTCAGAAACCCAGCTGAATCGCAACACC 183
DB 208 AACTGTAGTGTGCGCTTCTCTGTTTCAGAAACCCAGCTGAATCGCAACACC 267
QY 184 GGTAAACGACGATATCATCAAGTTTCATTAAAACTGAAACGTAACCGCGCTCC 243
DB 268 GGAACCAATGAAAGATATCAATGTATCAATTAATAAGCTGAAGAGAAACCACTTCC 327
QY 244 ACCAAGCGAGTGTGCTCAGAAAACCGTCTGACCCCGCTGTTGATTTATGAG 303
DB 328 ACAATGTGAGGAGGAGAAACAGAAACAGACTAATCATGCTTATGTGATTTATGAG 387
QY 304 AAAAATTTATGTAATGACCTGTTTCAGAAACCCAGCTGAATCGCAACACC 363
DB 388 AAAAATTTATGTAATGACCTGTTTCAGAAACCCAGCTGAATCGCAACACC 447
QY 364 CAGCACCTGTCTCTGTTACCAAGTTCCGAAGATTCCTGA 405
DB 448 CAGCATCTGTCTCTGTTACCAAGTTCCGAAGATTCCTGA 489

RESULT 2
CD559455/c 566 bp mRNA linear EST 11-JUN-2003
LOCUS AGENCOURT 14497025 NIH MGC 195 Homo sapiens CDNA clone
DEFINITION IMAGE:6971867 3', mRNA sequence.

ACCESSION CD559455 GI:31585523
VERSION CD559455.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 566)
REFERENCE NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgsabs-remail.nih.gov
Tissue Procurement: Narayan Bhat
CDNA Library Preparation: Bhat Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: IRBK2 row: 9 column: 10
High quality sequence stop: 566.
Location/Qualifiers
1. 566
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971867"
/issue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_1lb="NIH_MGC_195"

FEATURES
source

/note="Vector: pDNR-Dual; Site 1: loxp-SalI; Site 2: loxp-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxp sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearranged_plates/IRBK.presv.dat
a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 74.0%; Score 299.6; DB 5; Length 566;
Best Local Similarity 84.1%; Pred. No. 9, 8e-83;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 4 CAAGGTCAAGATCGCCATGATTTAGAAATCGTCACTTATAGATATTTGATCAGCTG 63
DB 433 CAAGGTCAAGATCGCCATGATTTAGAAATCGTCACTTATAGATATTTGATCAGCTG 374
QY 64 AAAAATTTATGTAATGACCTGTTCCGGAATTCCTGCGGCTCCGGAAGATGTTAGACC 123
DB 373 AAAAATTTATGTAATGACCTGTTCCGGAATTCCTGCGGCTCCGGAAGATGTTAGACC 314
QY 124 AACTGTAGTGTGCGCTTCTCTGTTTCAGAAACCCAGCTGAATCGCAACACC 183
DB 313 AACTGTAGTGTGCGCTTCTCTGTTTCAGAAACCCAGCTGAATCGCAACACC 254
QY 184 GGTAAACGACGATATCATCAAGTTTCATTAAAACTGAAACGTAACCGCGCTCC 243
DB 253 GGAACCAATGAAAGATATCAATGTATCAATTAATAAGCTGAAGAGAAACCACTTCC 194
QY 244 ACCAAGCGAGTGTGCTCAGAAAACCGTCTGACCCCGCTGTTGATTTATGAG 303
DB 193 ACAATGTGAGGAGGAGAAACAGAAACAGACTAATCATGCTTATGTGATTTATGAG 134
QY 304 AAAAATTTATGTAATGACCTGTTTCAGAAACCCAGCTGAATCGCAACACC 363
DB 133 AAAAATTTATGTAATGACCTGTTTCAGAAACCCAGCTGAATCGCAACACC 74
QY 364 CAGCACCTGTCTCTGTTACCAAGTTCCGAAGATTCCTGA 405
DB 73 CAGCATCTGTCTCTGTTACCAAGTTCCGAAGATTCCTGA 32

RESULT 3
CD559609 573 bp mRNA linear EST 26-NOV-2003
LOCUS AGENCOURT 14496932 NIH MGC 195 Homo sapiens CDNA clone
DEFINITION IMAGE:6971866 5', mRNA sequence.

ACCESSION CD559609 GI:38558943
VERSION CD559609.2
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 573)
REFERENCE NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585677.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Narayan Bhat
 CDNA Library Preparation: Bhat Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>
 Plate: IRBK2 row: 9 column: 09
 High quality sequence stop: 573.

FEATURES

source

1. 573
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6971866"
 /tissue_type="mixed"
 /lab_host="DH5A (T1 phage-resistant)"
 /clone_lib="NIH MGC 195"
 /note="Vector: PDNR-Dual; Site 1: loxp-Sall; Site 2:
 loxp-HindIII; Clones from this library have been
 PCR-amplified using gene-specific primers to contain the
 complete open reading frame (based on known gene sequences
 available from NCBI's RefSeq). Template for PCR is cDNA
 derived from either pooled cytoplasmic polyA RNA from 30
 cells lines or pooled total RNA from 10 different tissues
 (from BD Biosciences/Clontech and Washington University).
 PCR products are directionally cloned into the loxp sites
 of the PDNR-Dual vector. Library constructed by Dr.
 Narayan Bhat, Earl Bere III and Hongling Liao (Gene
 Expression Laboratory, Research Technology Program, SAIC
 Frederick, NCI-Frederick, Frederick, MD 21702). For
 information on which gene each clone represents, please
 visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
 a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 74.0%; Score 299.6; DB 5; Length 573;
 Best Local Similarity 84.1%; Pred. No. 9.9e-83;
 Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

```

QY 4 CAAGTCAAGTCCGACATGATTAAGATGGCTCACTTATAGATTTGTTGATCAGCTG 63
   |||||
Db 139 CAAGTCAAGATCCGACATGATTAAGATGGCTCACTTATAGATTTGTTGATCAGCTG 198
QY 64 AAAAATTATGTAATGACCTGGTCCGGAATTCGCGCGGCTCCGGAAGATGTGAGACC 123
   |||||
Db 199 AAAAATTATGTAATGACCTGGTCCGGAATTCGCGCGGCTCCGGAAGATGTGAGACA 258
QY 124 AACTGTAGTGTGCGCTTCTCTGTTTCCAGAAAGCCAGCTGAATCCGCAACACC 183
   |||||
Db 259 AACTGTAGTGTGCGCTTCTCTGTTTCCAGAAAGCCAGCTGAATCCGCAACACC 318
QY 184 GGTACCAACGAGTATCATCAAGTTTCCATTAAAAAGTGAACGTAACCGCGCTCC 243
   |||||
Db 319 GGAACCAATGAAGATATCAATGTATTAAGCTGAAGAGGAAACCACTTCC 378
QY 244 ACCAAGCGAGGTGCTCGTCAAGAAACCGCTGACCTGCGGCTCTGTGATTTATAGAG 303
   |||||
Db 379 ACAATATGAGGAGAAACGAAACACAGACTTAACGCTTCACTGATTTATAGAG 438
QY 304 AAAAAACCGCGAAAGATTCCTGTGAAAGTTTCAATCCCTGTGCGAAGAAATGATTCAC 363
   |||||
Db 439 AAAAAACCGCGAAAGATTCCTGTGAAAGTTTCAATCCCTGTGCGAAGAAATGATTCAT 498
QY 364 CAGCACTGTCTCTCTGTAACCAAGGTTCCGAAGATTCCTGA 405
   |||||
Db 499 CAGCATCTGTCTCTAGAACACAGCGAAGTGAAGATTCCTGA 540

```

RESULT 4

CD559459/c
 LOCUS CD559459 581 bp mRNA linear EST 19-NOV-2003
 DEFINITION AGENCOURT 14496771 NIH MGC_195 Homo sapiens cDNA clone
 IMAGE:6971863 5', mRNA sequence.
 ACCESSION CD559459
 VERSION CD559459.2 GI:38453485
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominoidea; Homo.
 1 (bases 1 to 581)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 On Jun 10, 2003 this sequence version replaced gi:31585527.
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Narayan Bhat
 CDNA Library Preparation: Bhat Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>
 Plate: IRBK2 row: 9 column: 06
 High quality sequence start: 21
 High quality sequence stop: 581.
 Location/Qualifiers

FEATURES

source

1. 581
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6971863"
 /tissue_type="mixed"
 /lab_host="DH5A (T1 phage-resistant)"
 /clone_lib="NIH MGC 195"
 /note="Vector: PDNR-Dual; Site 1: loxp-Sall; Site 2:
 loxp-HindIII; Clones from this library have been
 PCR-amplified using gene-specific primers to contain the
 complete open reading frame (based on known gene sequences
 available from NCBI's RefSeq). Template for PCR is cDNA
 derived from either pooled cytoplasmic polyA RNA from 30
 cells lines or pooled total RNA from 10 different tissues
 (from BD Biosciences/Clontech and Washington University).
 PCR products are directionally cloned into the loxp sites
 of the PDNR-Dual vector. Library constructed by Dr.
 Narayan Bhat, Earl Bere III and Hongling Liao (Gene
 Expression Laboratory, Research Technology Program, SAIC
 Frederick, NCI-Frederick, Frederick, MD 21702). For
 information on which gene each clone represents, please
 visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
 a Note: this is a NIH_MGC Library."

ORIGIN

Query Match 74.0%; Score 299.6; DB 5; Length 581;
 Best Local Similarity 84.1%; Pred. No. 9.9e-83;
 Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

```

QY 4 CAAGTCAAGTCCGACATGATTAAGATGGCTCACTTATAGATTTGTTGATCAGCTG 63
   |||||
Db 448 CAAGTCAAGATCCGACATGATTAAGATGGCTCACTTATAGATTTGTTGATCAGCTG 389
QY 64 AAAAATTATGTAATGACCTGGTCCGGAATTCCTGCGGCTCCGGAAGATGTGAGACC 123
   |||||
Db 388 AAAAATTATGTAATGACCTGGTCCGGAATTCCTGCGGCTCCGGAAGATGTGAGACA 329
QY 124 AACTGTAGTGTGCGCTTCTCTGTTTCCAGAAAGCCAGCTGAAGATCCGCAACACC 183

```

|||||
Db 328 AACTGTAGTGTAGCTTTTCTCTGTTTTCAGAGGCCCACTAAAGTCAGCAAAATACA 269
Qy 184 GGTAAACAGACGATCATCAACGTTTCCATTAAATACTGAAACCGCCGCTCC 243
Db 268 GGAACCAATGAAAGATTAATCAATGATCAATTAAGAGGAGGAAACCACTTCC 209
Qy 244 ACCAAGCAGAGTGTGTGTCAGAAACCGTGTGACCGCCGTCCTGTGATTCATTAG 303
Db 208 ACAAAATGCAAGAGACAGAAACAGACATTAATGATCCCTTATGATTCATTATAG 149
Qy 304 AAAAAACCGCCGAAAGAAATTCCTGGAACGTTTCAATCCCTGTGTCAGAAATGATTCAC 363
Db 148 AAAAAACCAACCAAGAAATTCCTGAAAGAAATTCATCAATTCCTCAAAAAGATTCAT 89
Qy 364 CAGCACTGTCTCTCTGTCACCAAGGTTCCGAGATTCCTGA 405
Db 88 CAGCATCTGTCTCTAGAACACAGGAAGTGAAGATTCCTGA 47

RESULT 5
CD559457/c 582 bp mRNA linear EST 19-NOV-2003
LOCUS AGENCOURT 14496897 NIH_MGC_195 Homo sapiens cDNA clone
ACCESSION CD559457 IMAGE:6971865 5', mRNA sequence.
VERSION CD559457.2 GI:38453482
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo
1 (bases 1 to 582)
NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585525.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
CDNA Library Preparation: Bhat Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
plate: IRBK2 row: 9 column: 08
High quality sequence start: 5
High quality sequence stop: 582.
Location/Qualifiers
1. 582

FEATURES
source
1. 582
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971865"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/note="Vector: pDNR-Dual; Site 1: loxP-Sall; Site 2:
loxP-HindIII; Clones from this library have been
PCR-amplified using gene-specific primers to contain the
complete open reading frame (based on known gene sequences
available from NCBI's RefSeq). Template for PCR is cDNA
derived from either pooled cytoplasmic polyA RNA from 30
cells lines or pooled total RNA from 10 different tissues
(from BD Biosciences/Clontech and Washington University).
PCR products are directionally cloned into the loxP sites
of the pDNR-Dual vector. Library constructed by Dr.
Narayan Bhat, Earl Bere III and Hongling Liao (Gene

Expression Laboratory, Research Technology Program, SAIC
Frederick, NCI-Frederick, Frederick, MD 21702). For
information on which gene each clone represents, please
visit our anonymous ftp site at
ftp://image.llnl.gov/image/retrayed_plates/IRBK-presv.dat
a Note: this is a NIH_MGC Library."

ORIGIN
Query Match 74.0%; Score 299.6; DB 5; Length 582;
Best Local Similarity 84.1%; Pred. No. 9.9e-83;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
Qy 4 CAAGTCAAGATGCCCATGATTAGATCGTCAACTTAATATTTGATCACTG 63
Db 449 CAAGTCAAGATGCCCATGATTAGATCGTCAACTTAATATTTGATCACTG 390
Qy 64 AAAAAATTATGTGAATGACTGTTCCGGAATTCCTGCGGCTCCGAAATGTTGAGACC 123
Db 389 AAAAAATTATGTGAATGACTGTTCCGGAATTCCTGCGGCTCCGAAATGTTGAGACA 330
Qy 124 AACTGTAGTGTGTCCTCTCTGTTTCCAGAAAGCCAGCTGAATCCGAAACACC 183
Db 329 AACTGTAGTGTGTCCTCTCTGTTTCCAGAAAGCCAGCTGAATCCGAAACACC 270
Qy 184 GGTAAACAGACGATCATCAACGTTTCCATTAAATACTGAAACCGCCGCTCC 243
Db 268 GGAACCAATGAAAGATTAATCAATGATCAATTAAGAGGAGGAAACCACTTCC 210
Qy 244 ACCAAGCAGAGTGTGTGTCAGAAACCGTGTGACCGCCGTCCTGTGATTCATTAG 303
Db 209 ACAAAATGCAAGAGACAGAAACAGACATTAATGATCCCTTATGATTCATTATAG 150
Qy 304 AAAAAACCGCCGAAAGAAATTCCTGGAACGTTTCAATCCCTGTGTCAGAAATGATTCAC 363
Db 148 AAAAAACCAACCAAGAAATTCCTGAAAGAAATTCATCAATTCCTCAAAAAGATTCAT 90
Qy 364 CAGCACTGTCTCTCTGTCACCAAGGTTCCGAGATTCCTGA 405
Db 89 CAGCATCTGTCTCTAGAACACAGGAAGTGAAGATTCCTGA 48

RESULT 6
CD559461/c 582 bp mRNA linear EST 19-NOV-2003
LOCUS AGENCOURT 14496648 NIH_MGC_195 Homo sapiens cDNA clone
DEFINITION IMAGE:6971861 5', mRNA sequence.
ACCESSION CD559461
VERSION CD559461.2 GI:38453488
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo
1 (bases 1 to 582)
NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT On Jun 10, 2003 this sequence version replaced gi:31585529.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
CDNA Library Preparation: Bhat Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
plate: IRBK2 row: 9 column: 04
High quality sequence start: 7

FEATURES

High quality sequence stop: 582.

Location/Qualifiers

```

1..582
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971861"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_id="NIH_MGC_195"
/notes="Vector: pDNR-Dual; Site 1: loxp-Sall; Site 2: loxp-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxp sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
a Note: this is a NIH_MGC Library."

```

ORIGIN

Query Match 74.0%; Score 299.6; DB 5; Length 582;
 Best Local Similarity 84.1%; Pred. No. 9.9e-83;
 Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

```

QY 4 CAAGGTCAAGATCGGCACATGATTTAGAAATGCGTCACTTAATGATTTGTTGATCAGCTG 63
DB 449 CAAGGTCAAGATCGGCACATGATTTAGAAATGCGTCACTTAATGATTTGTTGATCAGCTG 390
QY 64 AAAAATTATGTAATGATGACCTGGTCCGGAATTCCTGCGGCTCCGGAAGATTGAGACC 123
DB 389 AAAAATTATGTAATGATGATGGTCCCTGAATTTCTGCAGCTCCAGAAAGATTAGAGACA 330
QY 124 AACTGTGATGTCGCTTCCTGCTTCCGAAAGCCGAGCTGAAATCCGCAAAACCC 183
DB 329 AACTGTGATGTCGCTTCCTGCTTCCGAAAGCCGAGCTGAAATCCGCAAAACCC 270
QY 184 GGTAAACAAGAACGATCATCAACGTTCCATTAATAAAGTAAACGCGCTCC 243
DB 269 GGAACCAATGAAGATATCAATATCAATTAATAAAGTAAACGCGCTCC 210
QY 244 ACCAAGCGAGTGTGTCAGAAACCGCTGACCTGCTGCTGATTTATGAG 303
DB 209 ACAATGACGAGGAGAAACAGAAACACAGACTAATGCTTCATGATTTATGAG 150
QY 304 AAAAAACCGCGGAAGATTTCTGGAAGCTTCAATCCCTGCTCAGAAATGATTCAC 363
DB 149 AAAAAACCGCGGAAGATTTCTGGAAGCTTCAATCCCTGCTCAGAAATGATTCAT 90
QY 364 CAGCACGTCGCTCTGTCAGCAAGGTTCCGAAAGTTCTTGA 405
DB 89 CAGCATCTGCTCTTGAACACACGGAAGTGAAGATTCCTGA 48

```

RESULT 7

CD559456/c 583 bp mRNA linear EST 19-NOV-2003
 LOCUS AGENCOURT_14496960 NIH_MGC_195 Homo sapiens cDNA clone
 DEFINITION IMAGE:6971866 5', mRNA sequence.
 ACCESSION CD559456
 VERSION CD559456.2 GI:38453480
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT On Jun 10, 2003 this sequence version replaced gi:31585524.
 Contract: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgaabp-remail.nih.gov
 Tissue Procurement: Narayan Bhat

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo
 1 (bases 1 to 583)
 NIH-MGC http://mgc.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 On Jun 10, 2003 this sequence version replaced gi:31585524.
 Contract: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgaabp-remail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: Bhat Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: IRBK2 row: 9 column: 09
 High quality sequence start: 8
 High quality sequence stop: 583.
 Location/Qualifiers

FEATURES

source

```

1..583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971866"
/tissue_type="mixed"
/lab_host="DH5A (T1 phage-resistant)"
/clone_id="NIH_MGC_195"
/notes="Vector: pDNR-Dual; Site 1: loxp-Sall; Site 2: loxp-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxp sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBK.presv.dat
a Note: this is a NIH_MGC Library."

```

ORIGIN

Query Match 74.0%; Score 299.6; DB 5; Length 583;
 Best Local Similarity 84.1%; Pred. No. 9.9e-83;
 Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

```

QY 4 CAAGGTCAAGATCGGCACATGATTTAGAAATGCGTCACTTAATGATTTGTTGATCAGCTG 63
DB 450 CAAGGTCAAGATCGGCACATGATTTAGAAATGCGTCACTTAATGATTTGTTGATCAGCTG 391
QY 64 AAAAATTATGTAATGATGACCTGGTCCGGAATTCCTGCGGCTCCGGAAGATTGAGACC 123
DB 390 AAAAATTATGTAATGATGATGGTCCCTGAATTTCTGCAGCTCCAGAAAGATTAGAGACA 331
QY 124 AACTGTGATGTCGCTTCCTGCTTCCGAAAGCCGAGCTGAAATCCGCAAAACCC 183
DB 330 AACTGTGATGTCGCTTCCTGCTTCCGAAAGCCGAGCTGAAATCCGCAAAACCC 271
QY 184 GGTAAACAAGAACGATCATCAACGTTCCATTAATAAAGTAAACGCGCTCC 243
DB 270 GGAACCAATGAAGATATCAATATCAATTAATAAAGTAAACGCGCTCC 211
QY 244 ACCAAGCGAGTGTGTCAGAAACCGCTGACCTGCTGCTGATTTATGAG 303
DB 210 ACAATGACGAGGAGAAACAGAAACACAGACTAATGCTTCATGATTTATGAG 151

```

QY 304 AAAAAACCGCGAAGAATTCTGGAACGTTTCAATCCCTGCGAGAAAATGATTAC 363
 DB 150 AAAAAACCGCGAAGAATTCTGGAACGTTTCAATCCCTGCGAGAAAATGATTAC 91
 QY 364 CAGACCTGTCTCTCTGTAACCAAGTTCGGAAGATTCTCTGA 405
 DB 90 CAGCATCTGTCTCTTACACACAGGAAGGAATTCTCTGA 49

RESULT 8
 CDS59612 583 bp mRNA linear EST 26-NOV-2003
 LOCUS AGENCOURT_14496744 NIH_MGC_195 Homo sapiens cDNA clone
 DEFINITION IMAGE:69711863 5', mRNA sequence.
 ACCESSION CDS59612
 VERSION CDS59612.2 GI:38558948
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 REFERENCE 1 (bases 1 to 583)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT On Jun 10, 2003 this sequence version replaced gi:31585680.
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: Bhat Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: IRBK2 row: 9 column: 06
 High quality sequence stop: 583.
 Location/Qualifiers
 1..583
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6971863"
 /tissue_type="mixed"
 /lab_host="DH5A (TI phage-resistant)"
 /clone_lib="NIH MGC_195"
 /note="Vector: pDNR-Dual; Site 1: loxp-Sall; Site 2:
 loxp-HindIII; Clones from this library have been
 PCR-amplified using gene-specific primers to contain the
 complete open reading frame (based on known gene sequences
 available from NCBI's RefSeq). Template for PCR is cDNA
 derived from either pooled cytoplasmic polyA RNA from 30
 cells lines or pooled total RNA from 10 different tissues
 (from BD Biosciences/Clontech and Washington University).
 PCR products are directionally cloned into the loxp sites
 of the pDNR-Dual vector. Library constructed by Dr.
 Narayan Bhat, Earl Bere III and Hongling Liao (Gene
 Expression Laboratory, Research Technology Program, SAIC
 Frederick, NCI-Frederick, Frederick, MD 21702). For
 information on which gene each clone represents, please
 visit our anonymous ftp site at
 ftp://image.llnl.gov/image/rearrayed_plates/IRBK_presv.dat
 a Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 74.0%; Score 299.6; DB 5; Length 583;
 Best Local Similarity 84.1%; Pred. No. 9.9e-83;
 Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 4 CAAGTCAAGATCGCCACATGATTAGAAATGCGTCAACTTATGATTTGATCAGCTG 63
 DB 151 CAAGTCAAGATCGCCACATGATTAGAAATGCGTCAACTTATGATTTGATCAGCTG 210
 QY 64 AAAAAATTATGTGAATGACTGTTCCGAAATTCCTGCGGCTCCGGAAGATTGAGACC 123
 DB 211 AAAAAATTATGTGAATGACTGTTCCGAAATTCCTGCGGCTCCGGAAGATTGAGACC 270
 QY 124 AACTGTGAGTGTGCGGCTTTCTCTGTTTCCAGAAAGCCAGTGAATCCGAAAGACC 183
 DB 271 AACTGTGAGTGTGCGGCTTTCTCTGTTTCCAGAAAGCCAGTGAATCCGAAAGACC 330
 QY 184 GGTATCAAGCAAGTATCATCAAGTTTCCATTAAAAAGCTGAACCGCCGCTCC 243
 DB 331 GGAATCATGAAGATATCATATGATTAATTAAGCTGAAGAGAAACACGCTTCC 390
 QY 244 ACCAAGCAGGTGCTGCTGAGAAACACCGTCTGACTGCGGCTGTTGATTTATGAG 303
 DB 391 ACAATGCAGGAGAAAGACAGAAACACAGACTAATCATGCTTATGATTTATGAG 450
 QY 304 AAAAAACCGCGAAGAATTCTGGAACGTTTCAATCCCTGCGAGAAAATGATTAC 363
 DB 451 AAAAAACCGCGAAGAATTCTGGAACGTTTCAATCCCTGCGAGAAAATGATTAC 510
 QY 364 CAGACCTGTCTCTCTGTAACCAAGTTCGGAAGATTCTCTGA 405
 DB 511 CAGCATCTGTCTCTTACACACAGGAAGGAATTCTCTGA 552

RESULT 9
 CDS59614 592 bp mRNA linear EST 26-NOV-2003
 LOCUS AGENCOURT_14496629 NIH_MGC_195 Homo sapiens cDNA clone
 DEFINITION IMAGE:69711861 5', mRNA sequence.
 ACCESSION CDS59614
 VERSION CDS59614.2 GI:38558951
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 REFERENCE 1 (bases 1 to 592)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT On Jun 10, 2003 this sequence version replaced gi:31585682.
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: Bhat Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: IRBK2 row: 9 column: 04
 High quality sequence stop: 592.
 Location/Qualifiers
 1..592
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6971861"
 /tissue_type="mixed"
 /lab_host="DH5A (TI phage-resistant)"
 /clone_lib="NIH MGC_195"
 /note="Vector: pDNR-Dual; Site 1: loxp-Sall; Site 2:
 loxp-HindIII; Clones from this library have been

FEATURES
 source

LOCUS CD559613 600 bp mRNA linear EST 26-NOV-2003
 DEFINITION AGENCOURT 14496682 NIH_MGC_195 Homo sapiens cDNA clone
 ACCESSION CD559613
 VERSION CD559613.2 GI:38558920
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 600)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT On Jun 10, 2003 this sequence version replaced gi:31585681.
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: Bhat Laboratory
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: IRBK2 row: 9 column: 05
 High quality sequence start: 14
 High quality sequence stop: 600.
 Location/Qualifiers
 1..600
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6971862"
 /issue_type="mixed"
 /lab_host="DH5A (T1 phage-resistant)"
 /clone_id="NIH_MGC_195"
 /note="Vector: PDNR-Dual; Site_1: loxp-sali; Site_2: loxp-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxp sites of the PDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at
 ftp://image.llnl.gov/image/rearayed_plates/IRBK.presv.dat
 a Note: this is a NIH_MGC library."

ORIGIN
 Query Match 73.6%; Score 298; DB 5; Length 600;
 Best Local Similarity 83.8%; Pred. No. 3.2e-82;
 Matches 337; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

4 CAAGTCAGAGTCCGACATGATTAGAAATGCGTCACTTATGATTTGATCAGCTG 63
 166 CAAGGTCAAGATCCGACATGATTAGAAATGCGTCACTTATGATTTGATCAGCTG 225
 64 AAAAAATATGATGACCTGCTCCGGAATTCCTGCGGCTCCGGAAGATTTGAAC 123
 226 AAAAAATATGATGACCTGCTCCGGAATTTTCGCAAGTTCGCAAGAGTGAAGCA 285
 124 AACTGTAGTGTGCGCTTTCTCGTTTCCAGAAAGCCGCTGAATCCGCAACACC 183

Db 286 AACTGTAGTGTGTCAGCTTTTCTCGCTTCAGAAAGCCCACTAAATGACAAATACA 345
 Qy 184 GTTACAGACAGATGATCATCAAGCTTCCATTAAAAAGTAAAGCAACGCCCGTCC 243
 Db 346 GGAACCAATAGAAAGATTAATGATTAATTAAGCTGGAAGAGAAACCACTTCC 405
 Qy 244 ACCAAGCAGTGTGCTGTCAGAAACACCGTGTGACCTGCTGTGATTTCTTATGAG 303
 Db 406 ACAATGCAAGAGAAACAGAAACACAGACTAATGATGATGATTTATGAG 465
 Qy 304 AAAAAACCGCCGAAAGATTCCTGAAACGTTTCAATTCCTGCTGCGAAATATTCAC 363
 Db 466 AAAAAACCAACCAAGATTCCTGAAAGATTCCTGAAATGATTCCTGCAAAAGATTCAT 525
 Qy 364 CAGACCTGTCTCTGTACCAACCGTTCGAAAGATTCCTGA 405
 Db 526 CAGACTGTCTCTGATGACACAGGAAGTGAAGATTCCTGA 567

RESULT 12
 LOCUS CD559460/c 581 bp mRNA linear EST 19-NOV-2003
 DEFINITION AGENCOURT 14496710 NIH_MGC_195 Homo sapiens cDNA clone
 ACCESSION CD559460
 VERSION CD559460.2 GI:38453455
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 581)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT On Jun 10, 2003 this sequence version replaced gi:31585528.
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: Bhat Laboratory
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: IRBK2 row: 9 column: 05
 High quality sequence start: 4
 High quality sequence stop: 581.
 Location/Qualifiers
 1..581
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6971862"
 /issue_type="mixed"
 /lab_host="DH5A (T1 phage-resistant)"
 /clone_id="NIH_MGC_195"
 /note="Vector: PDNR-Dual; Site_1: loxp-sali; Site_2: loxp-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxp sites of the PDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bere III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC

This clone is available from RZPD;
<http://www.rzpd.de/cgi-bin/products/ci.cgi?cloneid=RZPD90160144>
 contact RZPD (product-support@rzpd.de) for further information.
 Primer name: qe3_4, Primer sequence: CGGATACAAATTCACACAG.

FEATURES

SOURCE

Location/Qualifiers
 1..551

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="RZPD90160144"
 /issue_type="T-Lymphocytes"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_1id="RZPD no. 9016"
 /note="Vector: pQE80LSN_cloned; Site_1: SalI; Site_2:
 NotI; vector:
http://www.rzpd.de/info/vectors/pQE80LSN_cloned_pic.shtml
 ; 1st strand cDNA was prepared from mRNA obtained from
 human T-Lymphocytes with a NotI - oligo(dT) primer [5',
 GACTAGTCTTAGATCGGAGCGGCCCTTTTCTTTTCTTTT 3'].
 Double-stranded cDNA was ligated to SalI adaptors,
 digested with NotI and cloned into the NotI and SalI sites
 of the pQE80LSN_cloned vector"

ORIGIN

Query Match 72.2%; Score 292.6; DB 8; Length 551;
 Best Local Similarity 82.3%; Pred. No. 1.6e-80;
 Matches 331; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

4 CAAGGTCAAGTCCGCAATGATTAGAAATGCGTCACTTATGATTTGATCAGCTG 63
 139 CAAGGTCAAGTCCGCAATGATTAGAAATGCGTCACTTATGATTTGATCAGCTG 198
 64 AAAAATATGATGATGACCTGCTCCGAAATTCCTGCGGCTCCGGAAGATTTGAGACC 123
 199 AAAAATATGATGATGACCTGCTCCGAAATTCCTGCGGCTCCGGAAGATTTGAGACC 258
 124 AACTGTAGTGTGCTCGCTTTCTCCTGTTTCCAGAAAGCCAGCTGAATCCGCAAAACACC 183
 259 AACTGTAGTGTGCTCGCTTTCTCCTGTTTCCAGAAAGCCAGCTGAATCCGCAAAACACC 318
 184 GTTACACAGAAAGTATCATCAAGCTTTCATTAATAAAGTGAAGCTAAACCGCGCTCC 243
 319 GGAATCATGAAAGATATCAATGATTAATAAAGTGAAGCTAAACCGCGCTCC 378
 244 ACCAAGCAGTGTCTGCTGAGAAACACCTGTGACCTGCGGCTCCTGTGATTTTATGAG 303
 379 ACNAATCAGAGGAGAAAGACAGAAACACAGACTTAACATGCTTGTGATTTTATGAA 438
 304 AAAAATATGATGATGACCTGCTTTCTCCTGTTTCCAGAAAGCCAGCTGAATCCGCAAAACACC 363
 439 AAAAATATGATGATGACCTGCTTTCTCCTGTTTCCAGAAAGCCAGCTGAATCCGCAAAACACC 498
 364 CAGCAGCTGTCTCTGCTACCCACGCTTCGGAAGATTTCTGA 405
 499 CANNATCTGTCTCTTANACACAGCAAGTGAATATTCCTGA 540

RESULT 15
 CD559611 608 bp mRNA linear EST 26-NOV-2003
 LOCUS AGENCOURT 14496808 NIH MGC 195 Homo sapiens cDNA clone
 DEFINITION IMAGE:6971864 5', mRNA sequence.
 ACCESSION CD559611
 VERSION CD559611.2 GI:38558946
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 BUKARYOTA: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homindaes; Homo.
 REFERENCE 1 (bases 1 to 608)
 AUTHORS NIH-MGC <http://mgc.ncbi.nlm.nih.gov/>.

TITLE
 JOURNAL
 COMMENT

National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 On Jun 10, 2003 this sequence version replaced gi:31585679.
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics / NIH
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: Bhat Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>

FEATURES

SOURCE

Location/Qualifiers
 1..608

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6971864"
 /issue_type="mixed"
 /lab_host="DH5A (T1 phage-resistant)"
 /clone_1id="NIH MGC 195"
 /note="Vector: pDNR-Dual; Site_1: loxP-SalI; Site_2:
 loxP-HindIII; Clones from this library have been
 PCR-amplified using gene-specific primers to contain the
 complete open reading frame (based on known gene sequences
 available from NCBI's RefSeq). Template for PCR is cDNA
 derived from either pooled total RNA from 10 different tissues
 (cells lines or pooled total RNA from 10 different tissues
 (from BD Biosciences/Clontech and Washington University).
 PCR products are directionally cloned into the loxP sites
 of the pDNR-Dual vector. Library constructed by Dr.
 Narayan Bhat, Earl Bere III and Hongling Liao (Gene
 Expression Laboratory, Research Technology Program, SAIC
 Frederick, NCI-Frederick, Frederick, MD 21702). For
 information on which gene each clone represents, please
 visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearayed_plates/IRBK.presv.dat
 A Note: this is a NIH_MGC Library."

ORIGIN

Query Match 69.9%; Score 283.2; DB 5; Length 608;
 Best Local Similarity 82.7%; Pred. No. 1.5e-77;
 Matches 339; Conservative 0; Mismatches 63; Indels 8; Gaps 1;

4 CAAGGTCAAGTCCGCAATGATTAGAAATGCGTCACTTATGATTTGATCAGCTG 63
 166 CAAGGTCAAGTCCGCAATGATTAGAAATGCGTCACTTATGATTTGATCAGCTG 225
 64 AAAAATATGATGATGACCTGCTTTCTCCTGTTTCCAGAAAGCCAGCTGAATCCGCAAAACACC 123
 226 AAAAATATGATGATGACCTGCTTTCTCCTGTTTCCAGAAAGCCAGCTGAATCCGCAAAACACC 285
 124 AACTGTAGTGTGCTCGCTTTCTCCTGTTTCCAGAAAGCCAGCTGAATCCGCAAAACACC 183
 286 AACTGTAGTGTGCTCGCTTTCTCCTGTTTCCAGAAAGCCAGCTGAATCCGCAAAACACC 345
 184 GTTACACAGAAAGTATCATCAAGCTTTCATTAATAAAGTGAAGCTAAACCGCGCTCC 243
 346 GGAATCATGAAAGATATCAATGATTAATAAAGTGAAGCTAAACCGCGCTCC 405
 244 ACCAAGCAGTGTCTGCTGAGAAACACCTGTCTGCTGATTT 295
 406 ACAATCAGAGGAGAAAGACAGAAACACAGACTTAATTTCTGAGACATGCTTCATGATGATTT 465
 296 CTTATGAGAAAAACCGCGGAAGAAATCTTGAAAGCTTTCAATCCCTGTGTGAGAAAA 355
 466 CTTATGAGAAAAACCGCGGAAGAAATCTTGAAAGCTTTCAATCCCTGTGTGAGAAAA 525

Qy 356 TGATTCACCAAGACCTGTCTCTCGTACCCAGGTTCCGAAGATTCTTGA 405
|||||
Db 526 TGATTCATCAGCATCTGTCTCTAGAACACACGGAAGTGAAGATTCTTGA 575
|||||

Search completed: August 7, 2006, 13:37:22
Job time : 4434 secs

THIS PAGE LEFT BLANK